

A141736
F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220
F-NT2RM2000566//Integrin, alpha 7B/2.0e-155:751:97//Hs.74369:AF032108
F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508
5 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128
F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363: D86987
10 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220
F-NT2RM2000594
F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402: AF040963
F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313
15 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548
F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093
F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542: AB018272
20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558
F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702
F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763: AB014576
F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371
25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs. 5321:AF06083
F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984
F-NT2RM2000718//Homo sapiens mRNA for HRI/HFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342
F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244
30 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286
F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750
F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338
F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701
35 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylose kinase, complete cds//2.8e-185:847:99//Hs.137580: AB015046
F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075: AI023761
F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433
40 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831
F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs. 17035:AI080471
F-NT2RM2001065
F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449: 62//Hs.75111:D87258
F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds// 0.0079:274:59//Hs.102732:U88153
F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190
F-NT2RM2001141
50 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042
F-NT2RM2001177
F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:AI288739
F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959
F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630
55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349
F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766
F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928
F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

AF039694
F-NT2RM2001256
F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845
F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601
5 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615
F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:
AI138605
F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567
F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706
10 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905
F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322
F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382
F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378
F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:
15 AJ007509
F-NT2RM2001499//Ectotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303
F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903
F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:AA58969
F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459
20 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262
F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:
64//Hs.1042:M62800
F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077
F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902
25 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729
F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431
F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis
familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918
30 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:
AB014518
F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952
F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92://
Hs.22142:AA814725
35 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis
familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301
F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287
F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-
40 173:802:99//Hs.31323:AF044195
F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:
671:97//Hs.27721:U17907
F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:
AB011129
45 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356
F-NT2RM2001675
F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305
F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216
50 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937
F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415
F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817
F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//
0.95:270:61//Hs.15791:AF027262
55 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788
F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650
F-NT2RM2001718
F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

- F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530.98//Hs.129937:
AB007931
- F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269.58//Hs.129952:
AB011132
- 5 F-NT2RM2001743
F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350.59//Hs.100469:AB011399
- F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181.75//Hs.131840:AI016073
- F-NT2RM2001768//ESTs//0.61:189.62//Hs.144847:AI222742
- 10 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669.71//Hs.2479:X78933
- F-NT2RM2001782//YY1 transcription factor//0.094:149.65//Hs.97496:M77698
- F-NT2RM2001784//ESTs//8.2e-31:190.92//Hs.144587:AI193595
- F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476.74//Hs.132898:AC004770
- 15 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481.72//Hs.70617:D31763
- F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142.66//Hs.78202:
U29175
- F-NT2RM2001803//Homo sapiens ikappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-
179:827.99//Hs.31323:AF044195
- 20 F-NT2RM2001805//EST//1.0:45.80//Hs.159007:AI381341
F-NT2RM2001813//EST//0.41:268.58//Hs.150031:AI292068
- F-NT2RM2001823//H.sapiens mRNA for 218kD MI-2 protein//9.7e-21:554.60//Hs.74441:X86691
- F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738.90//Hs.7753:AF013759
- F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329.86//Hs.113283:AF190800
- 25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301.60//Hs.77541:M57567
F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421.66//Hs.8763:W30741
- F-NT2RM2001879//ESTs//6.3e-43:234.94//Hs.122546:AA186723
- F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866.97//Hs.4198:
AB014610
- 30 F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and
IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//3.0e-13:606.57//Hs.23170:AJ005892
- F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859.97//Hs.129937:
AB007931
- F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481.59//Hs.27621:
U52840
- 35 F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila mel-
anogaster]//0.37:424.60//Hs.118634:U66688
- F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653.98//Hs.21811:
AF091080
- 40 F-NT2RM2001950//ESTs//0.12:91.76//Hs.107295:W80392
F-NT2RM2001982
- F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:
AF089816
- F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319.59//Hs.104135:AJ006778
- 45 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538
F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271.60//Hs.63888:AA203398
- F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509.65//Hs.6214:AB018274
- F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429.58//Hs.79090:D89729
- F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822.73//Hs.1674:M90516
- 50 F-NT2RM2002049//ESTs//0.99:109.71//Hs.19303:AA28427
F-NT2RM2002055//ESTs//1.1e-91:453.98//Hs.158370:AI382154
- F-NT2RM2002088//ESTs//6.1e-75:302.96//Hs.153471:AI198377
- F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293.58//Hs.89631:U48508
- F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776.98//Hs.99423:
AJ010840
- F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-
145:684.98//Hs.26312:AF030435
- F-NT2RM2002128

F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274
 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:
 92//Hs.20815:AF084928
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:
 5 AB007936
 F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs.
 99936:X14487
 F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563
 F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074
 10 F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464
 F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674
 F-NT2RM4000061//ESTs//0.89:207:60//Hs.984474:AI038511
 F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H.
 15 sapiens]//1.6e-30:369:70//Hs.114623:AI204280
 F-NT2RM4000086
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865
 F-NT2RM4000139
 F-NT2RM4000155
 20 F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
 F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//
 Hs.159228:AF041853
 F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
 F-NT2RM4000191//TRICHONYALIN//0.011:324:60//Hs.82276:L09190
 25 F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
 F-NT2RM4000199//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322:
 61//Hs.145088:AI221147
 F-NT2RM4000200
 F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//HS.91400:
 30 AB006626
 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138:
 AB018255
 F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651
 F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458
 35 F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
 F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
 F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs.
 93841:AA442297
 F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs.
 40 46328:D87942
 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.
 31305:M99438
 F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:
 AB000712
 45 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707
 F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.
 12796:W27884
 F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630
 F-NT2RM4000354//ESTs, Weakly similar to lethal(2)deadlyless [D.melanogaster]//0.0078:55:92//Hs.59075:
 50 M023761
 F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542
 F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
 F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene
 55 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:
 843:68//Hs.23796:AL022718
 F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114.94//Hs.137580:
 AB015046
 F-NT2RM4000421
 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432.74//Hs.154872:
 5 AB011166
 F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543.58//Hs.2175:M59820
 F-NT2RM4000457
 F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178.631//Hs.
 66369:U95040
 10 F-NT2RM4000486//ESTs//9.2e-48:237.99//Hs.160685:AI280004
 F-NT2RM4000496//ESTs//0.069:252.61//Hs.155958:AA573632
 F-NT2RM4000511//EST//0.92:191.58//Hs.61517:AA028915
 F-NT2RM4000514
 15 F-NT2RM4000515//ESTs//7.3e-93:450.98//Hs.120975:AA034409
 F-NT2RM4000520//ESTs//0.13:183.65//Hs.144828:AI221305
 F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756.96//
 Hs.125870:AI364967
 F-NT2RM4000532//ESTs//7.7e-43:388.78//Hs.105665:H78987
 F-NT2RM4000534
 20 F-NT2RM4000585
 F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593.62//Hs.7764:
 AB007938
 F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III
 [Caenorhabditis elegans]//3.1e-104:532.96//Hs.6092:T75227
 25 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305.68//Hs.40100:AB002390
 F-NT2RM4000611//EST//0.76:268.58//Hs.150031:AI292068
 F-NT2RM4000616
 F-NT2RM4000674
 F-NT2RM4000689
 30 F-NT2RM4000698//Apolipoprotein E//1.0:290.59//Hs.76260:M12529
 F-NT2RM4000700
 F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744.77//Hs.
 42400:AF022789
 F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
 35 //2.6e-163:77.97//Hs.6823:W18181
 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257.60//Hs.857:M84605
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743.98//Hs.137168:
 AB018303
 F-NT2RM4000741
 40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388.96//Hs.
 112361:R99396
 F-NT2RM4000764//ESTs//3.8e-104:539.95//Hs.24739:H67815
 F-NT2RM4000778//ESTs//1.5e-85:419.97//Hs.99838:AA204731
 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810.98//Hs.18586:
 45 AB007920
 F-NT2RM4000787//EST//0.011:182.65//Hs.159928:AA969186
 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736.98//Hs.25817:AC005306
 F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-
 19:160.80//Hs.124902:AI337820
 50 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292.62//Hs.124212:M64676
 F-NT2RM4000798//ESTs//1.9e-34:271.82//Hs.128203:AA972301
 F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete
 cds//0.052:238.64//Hs.113265:AF032387
 F-NT2RM4000820//ESTs//0.053:274.61//Hs.23748:H16568
 55 F-NT2RM4000833
 F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374.61//Hs.7841:AB002322
 F-NT2RM4000852//EST//1.0:222.60//Hs.120354:AA718934
 F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapi-

ensi//4.4e-29: 164:95//Hs.115095:AI392943
 F-NT2RM4000887
 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004
 5 F-NT2RM4000950
 F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546
 F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875
 F-NT2RM4000996//Zinc finger protein 3 (A8-51) (8.7e-34:381:67//Hs.2481:X78926
 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:
 10 AB018272
 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:
 AB014539
 F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:
 AB018254
 15 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:
 AI247543
 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//
 0.79:142:69//Hs.77424:M63835
 F-NT2RM4001084
 20 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758
 F-NT2RM4001116
 F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701
 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730
 F-NT2RM4001155//ESTs//2.2e-18:171:74//Hs.128826:AI004145
 25 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351
 F-NT2RM4001187
 F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220
 F-NT2RM4001200//Zinc finger protein 10 (KOX 1) (4.0e-68:799:69//Hs.2479:X78933
 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs.
 30 14934:AF004828
 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME
 III [Caenorhabditis elegans]//1.9e-29:152:62//Hs.31582:AA877205
 F-NT2RM4001217//Homo sapiens nuclear matrix protein NRPB/B (NRPB) mRNA, complete cds//7.0e-63:715:70//
 Hs.104925:AF059611
 35 F-NT2RM4001258//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs.
 26676:AA033997
 F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360:
 AB007950
 F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003
 40 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973
 F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335
 F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016
 F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988
 F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTER-
 45 GENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714
 F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7
 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818
 F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656
 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:
 50 AF098799
 F-NT2RM4001384
 F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575
 F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520
 F-NT2RM4001412
 55 F-NT2RM4001414//ESTs, Moderately similar to 18547_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817
 F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087
 F-NT2RM4001444
 F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
 F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784
 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.151321:
 5 AB014585
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:
 AA456247
 F-NT2RM4001557
 10 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:
 25 55:60//Hs.14207:U86453
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859
 F-NT2RM4001582
 15 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566
 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:
 AB011094
 F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077
 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:
 20 AB018334
 F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739
 F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]
 //0.0042:153:88//Hs.114832:AI147946
 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339
 25 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320
 F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323
 F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638
 F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957
 30 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI32905
 F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903
 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318
 F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306
 F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//
 35 2.0e-27:205:83//Hs.116061:AA206719
 F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:
 X97630
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:
 AB018270
 40 F-NT2RM4001783//ESTs, Weakly similar to T12D8.1 [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677
 F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:
 446:58//Hs.27910:AF049105
 F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547
 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712
 45 F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:
 AI379442
 F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687
 F-NT2RM4001836//NUCLEOIBINDIN PRECURSOR//0.0022:588:59//Hs.953:M9624
 F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204
 50 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814
 F-NT2RM4001856
 F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete
 cds//8.0e-10:244:66//Hs.22138:U49250
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:
 55 Y17711
 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984
 F-NT2RM4001880
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

- F-NT2RM4001922//ESTs/2.5e-51:291:93//Hs.26660:AI312633
- F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:
AJ224875
- F-NT2RM4001938
- 5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:
AF098162
- F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087
- F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.
130135:AA05493
- 10 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862
- F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:
AB018341
- F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082
- F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936
- 15 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271
- F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601
- F-NT2RM4002034
- F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048
- F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912
- 20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:
AB014540
- F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]
//7.0e-94:396:94//Hs.59346:AI126802
- F-NT2RM4002063
- 25 F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:
AF071309
- F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040
- F-NT2RM4002073//Insulin-like growth factor binding protein 2/3.2e-10:470:61//Hs.162:X16302
- F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.
30 122967:AF059569
- F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) (alternative products)//9.2e-34:532:65//Hs.
146459:X66975
- F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.
69360:U63743
- 35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542
- F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877
- F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158
- F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:
AI037879
- 40 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535
- F-NT2RM4002174
- F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998
- F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:
U38276
- 45 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454
- F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182
- F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]
//8.4e-125:588:98//Hs.23900:U82984
- F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966
- 50 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764
- F-NT2RM4002266//Human kinase My1 (My1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118
- F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180
- F-NT2RM4002281
- F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
- 55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457
- F-NT2RM4002301
- F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331
- F-NT2RM4002339

F-NT2RM4002344//EST//0.16:166.64//Hs.128600:AA906454
 F-NT2RM4002373//*Homo sapiens* mRNA for KIAA0649 protein, complete cds//9.1e-151:708.98//Hs.26163:
 AB014549
 F-NT2RM4002374//*Homo sapiens* mRNA for KIAA0720 protein, partial cds//0.0040:303.63//Hs.23741:AB018263
 5 F-NT2RM4002383//ESTs//8.0e-16:153.78//Hs.155243:N70293
 F-NT2RM4002390
 F-NT2RM4002398
 F-NT2RM4002409
 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [*C.elegans*]//1.1e-55:282.96//Hs.
 10 26676:AA033997
 F-NT2RM4002446//*Homo sapiens* clone 24574 mRNA sequence//0.59:339.60//Hs.18686:AF052151
 F-NT2RM4002452
 F-NT2RM4002457//*Homo sapiens* mRNA for epiregulin, complete cds//3.2e-25:228.81//Hs.115263:D30783
 F-NT2RM4002460//EST//1.0:142.65//Hs.145370:AI252780
 15 F-NT2RM4002479//*Homo sapiens* RNA helicase-related protein mRNA, complete cds//8.9e-165:777.98//Hs.
 8765:AF083255
 F-NT2RM4002482//*Homo sapiens* mRNA for KIAA0691 protein, complete cds//7.3e-95:464.97//Hs.94781:
 AB014591
 F-NT2RM4002493
 20 F-NT2RM4002499//ESTs//1.3e-44:653.67//Hs.23790:N99347
 F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225.83//Hs.155464:AF088219
 F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290.60//Hs.154968:
 U02020
 F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232.61//Hs.82042:D87075
 25 F-NT2RM4002534//*Homo sapiens* angiotensin/vasopressin receptor All/AVP mRNA, complete cds//1.0:100.70//
 Hs.159483:AF054176
 F-NT2RM4002558//*Homo sapiens* amphiphysin II mRNA, complete cds//0.17:393.61//Hs.6619:U84004
 F-NT2RM4002565//*Homo sapiens* mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226.60//Hs.84043:
 D84273
 30 F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [*C.elegans*]//3.3e-88:484.93//Hs.105837:AA536054
 F-NT2RM4002571//ESTs, Weakly similar to UDP-CalNAc/polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121.70//Hs.155413:AA429394
 F-NT2RM4002593//ESTs//1.0e-15:103.95//Hs.108920:W28151
 F-NT2RM4002594//*Homo sapiens* 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:
 35 499.59:Hs.79357:D78275
 F-NT2RM4002623//ESTs//1.2e-11:92.92//Hs.164046:T97402
 F-NT2RP1000018//*Homo sapiens* mRNA for KIAA0687 protein, partial cds//2.0e-102:746.81//Hs.3628:AB014587
 F-NT2RP1000035//*Homo sapiens* mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747.96//Hs.159597:
 AJ012449
 40 F-NT2RP1000040//ESTs//1.3e-58:338.92//Hs.17534:H16907
 F-NT2RP1000063//ESTs//0.0013:72.83//Hs.108196:W81647
 F-NT2RP1000086//*Human* mRNA for KIAA0360 gene, partial cds//5.4e-185:548.91//Hs.79971:X98834
 F-NT2RP1000101//*Homo sapiens* hook2 protein (HOOK2) mRNA, complete cds//0.33:247.61//Hs.30792:
 AF044924
 45 F-NT2RP1000111
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324.81//Hs.2052:M86699
 F-NT2RP1000124//ESTs//2.4e-42:268.89//Hs.146078:AI084025
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:
 382.94//Hs.127842:W38901
 50 F-NT2RP1000163//*Homo sapiens* cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77.90//
 Hs.3760:AF011792
 F-NT2RP1000170//EST//0.68:130.63//Hs.146994:AI184430
 F-NT2RP1000174//*Homo sapiens* clone 24432 mRNA sequence//8.3e-140:679.97//Hs.78019:AF070535
 F-NT2RP1000191//ESTs//1.3e-71:405.93//Hs.24054:N46499
 55 F-NT2RP1000202//*H.sapiens* mRNA for cytokine inducible nuclear protein//2.0e-05:591.58//Hs.74019:X83703
 F-NT2RP1000243
 F-NT2RP1000259
 F-NT2RP1000272//*Homo sapiens* TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528.97//Hs.

- 4214.AF087730
 F-NT2RP1000324//ESTs/3.4e-98.499.96//Hs.42530:N41661
 F-NT2RP1000326//*Homo sapiens* metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148.693.98//Hs.31584:AF053551
 5 F-NT2RP1000333//*Homo sapiens* monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28.328.60//Hs.22405:AF004231
 F-NT2RP1000348//Human pliecin (PLEC1) mRNA, complete cds//0.018.337.62//Hs.79706:U53204
 F-NT2RP1000357
 F-NT2RP1000358//DYNAMIN-1//0.96.273.59//Hs.126:L07807
 10 F-NT2RP1000363//*Homo sapiens* mRNA for KIAA0638 protein, partial cds//3.2e-126.497.86//Hs.77864:AB014538
 F-NT2RP1000376//*Homo sapiens* calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178.877:96//Hs.120360:AF064594
 15 F-NT2RP1000409//ESTs//5.4e-59.415.83//Hs.140578:AA828031
 F-NT2RP1000413//*Homo sapiens* mRNA for KIAA0587 protein, complete cds//3.0e-179.710.98//Hs.21862:AB011159
 F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [*Mus musculus*]//7.3e-177.857.97//Hs.6823:W18181
 F-NT2RP1000418//*Homo sapiens* calcium-activated potassium channel (KCNN3)mRNA, complete cds//0.46.222:
 20 60//Hs.89230:AF031815
 F-NT2RP1000439//EST//0.98.339.56//Hs.137377:AA101603
 F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0.356.59//Hs.58435:AF001862
 F-NT2RP1000460
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:
 25 665.96//Hs.143187:AC002985
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57.440.80//Hs.159154:U47634
 F-NT2RP1000481//ESTs//4.8e-21.154.87//Hs.17392:AA535102
 F-NT2RP1000493
 30 F-NT2RP1000513//ESTs//2.2e-71.409.91//Hs.121029:AA480977
 F-NT2RP1000522//*Homo sapiens* clone DT1P1A11 mRNA, CAG repeat region//0.21.255.62//Hs.98834:U92992
 F-NT2RP1000547//*H.sapiens* mRNA for transmembrane protein mp24//1.9e-06.337.63//Hs.75914:X92098
 F-NT2RP1000574//*Homo sapiens* homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82.295.92//Hs.
 104105:AF017418
 35 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014.235.65//Hs.121552:J05213
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33.223.89//Hs.110802:X04385
 F-NT2RP1000609//*Homo sapiens* chromosome 11, BAC CIT-HSP-31ne8 (BC269730) containing the hFEN1 gene//2.2e-49.506.73//Hs.132898:AC004770
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19.556.62//Hs.
 40 152936:D63475
 F-NT2RP1000630
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05.389.59//Hs.3844:
 U24576
 F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43.232.95//Hs.3487:AA425553
 45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53.312.90//Hs.7049:
 AI141736
 F-NT2RP1000701//Myogenic factor 3//0.81.186.63//Hs.2834:AF027148
 F-NT2RP1000721//*Homo sapiens* mRNA for repressor protein, partial cds//4.0e-33.278.78//Hs.58167:D30612
 F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40.297.84//Hs.18122:AI338045
 50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31.286.78//Hs.2707:X17644
 F-NT2RP1000738//*Homo sapiens* Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete
 cds//2.6e-123.604.96//Hs.21771:AF101434
 F-NT2RP1000746
 F-NT2RP1000767
 55 F-NT2RP1000782//Human globin gene//3.6e-21.140.91//Hs.100090:M69023
 F-NT2RP1000796//*H.sapiens* mRNA for ROX protein//0.17.404.57//Hs.25497:X96401
 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for
 GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//

2.7e-23:147.91//Hs.102336.Z83838
 F-NT2RP1000833//*Homo sapiens* cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143.424:
 96//Hs.18953;AF067223
 5 F-NT2RP1000834//ESTs//0.18:280.60//Hs.157215.AI332903
 F-NT2RP1000836//EST//0.60:103.66//Hs.145708.AI267990
 F-NT2RP1000846//EST//1.2e-15:322.65//Hs.149925.AI288838
 F-NT2RP1000851//ESTs//6.1e-96:459.98//Hs.121586.AA423875
 F-NT2RP1000856//*Human* globin gene//6.7e-22:140.91//Hs.100090:M69023
 10 F-NT2RP1000860//*Homo sapiens* KLO4P mRNA, complete cds//2.2e-107:551.95//Hs.125156.AF064094
 F-NT2RP1000902//EST//1.8e-28:218.85//Hs.145258.AI218683
 F-NT2RP1000915//ESTs//8.8e-11:102.81//Hs.163740.AI248847
 F-NT2RP1000916//ESTs, Weakly similar to coded for by *C. elegans* cDNA cm04e9 [*C. elegans*]//2.2e-27:159.94//
 Hs.122153.AA780270
 F-NT2RP1000943//*Human* hSIAH2 mRNA, complete cds//0.45:130.68//Hs.20191.U76248
 15 F-NT2RP1000944//EST//0.99:116.63//Hs.116633.AA668400
 F-NT2RP1000947//*Human* E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:
 185.87//Hs.108332.U39317
 F-NT2RP1000954//*Homo sapiens* BACH1 mRNA, complete cds//0.81:329.56//Hs.154276.AB002803
 F-NT2RP1000956//ESTs//1.3e-20:129.92//Hs.163740.AI248847
 20 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76.73//Hs.73742.M17885
 F-NT2RP1000966//NUCLEOLIN//1.2e-72:353.98//Hs.79110.M60858
 F-NT2RP1000980//ESTs//1.6e-109:555.96//Hs.84429.N28866
 F-NT2RP1000988//*Human* chromosome 3p21.1 gene sequence//2.6e-73:665.80//Hs.82837.L13435
 F-NT2RP1001011
 25 F-NT2RP1001013//ESTs//3.4e-40:393.74//Hs.120206.AI089163
 F-NT2RP1001014
 F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313.59//Hs.150785.M61764
 F-NT2RP1001073//Glucocorticoid receptor//1.0:204.61//Hs.75772.M10901
 F-NT2RP1001079//ESTs//1.0:174.62//Hs.158209.AI360531
 30 F-NT2RP1001080//*Homo sapiens* forkhead protein (FKHL1) mRNA, complete cds//0.57:215.64//Hs.14845:
 AF032866
 F-NT2RP1001113//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEESB82F [*C. elegans*]//1.4e-65.293:
 95//Hs.32751.H38087
 F-NT2RP1001173
 35 F-NT2RP1001177//*Homo sapiens* histone macroH2A1.2 mRNA, complete cds//6.1e-26:259.74//Hs.75258:
 AF054174
 F-NT2RP1001185//EST//1.4e-27:266.77//Hs.122245.AA781524
 F-NT2RP1001199//ESTs//0.97:75.73//Hs.131498.AI022150
 F-NT2RP1001247//*Human* endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120.95//Hs.
 40 25195.U81523
 F-NT2RP1001248//ESTs//3.0e-21:143.93//Hs.157243.AI337094
 F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344.93//Hs.3090:
 AJ002231
 F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392.57//Hs.5541.Y15724
 45 F-NT2RP1001294
 F-NT2RP1001302
 F-NT2RP1001310//*Homo sapiens* creatine transporter mRNA, complete cds//3.6e-07:379.61//Hs.154503.U36341
 F-NT2RP1001311//ESTs//9.5e-37:403.93//Hs.24739.H67815
 F-NT2RP1001313//*Homo sapiens* chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1
 50 gene//3.1e-87:437.97//Hs.132898.AC004770
 F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tauri]//6.8e-101:480.94//Hs.75017.AA166853
 F-NT2RP1001385//EST//0.86:127.65//Hs.156304.AI336859
 F-NT2RP1001395//*Homo sapiens* stanni mRNAs, complete cds//0.75:355.58//Hs.76691.AF070673
 55 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157.63//Hs.89887.D38081
 F-NT2RP1001424//ESTs//5.3e-20:118.95//Hs.159782.R60700
 F-NT2RP1001432//ESTs//5.3e-20:118.95//Hs.159792.R60700
 F-NT2RP1001449//*Homo sapiens* clone 24733 mRNA sequence//5.7e-86:422.97//Hs.21970.AF052149

F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
 F-NT2RP1001466
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
 F-NT2RP1001482
 5 F-NT2RP1001494
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277
 F-NT2RP1001569
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913
 10 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:
 AF091081
 F-NT2RP2000006//ESTs, Weakly similar to B0035. 14 [C.elegans]//8.2e-47:300:89//Hs.6473:AA853955
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390
 15 F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
 2.0e-26:214:82//Hs.140385:AA773359
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.13019:AI038867
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290
 20 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//
 7.8e-97:467:97//Hs.6216:AF061749
 F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.
 158991:X54134
 25 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene
 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:
 767.61/Hs.23796:AL022718:F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203c13 (LBNL H155),
 complete sequence//6.5e-08:344:58//Hs.159402:AC005609
 30 F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.
 54877:AF050078
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:
 35 AB018338
 F-NT2RP2000091
 F-NT2RP2000097
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390
 40 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:
 AB018356
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
 [C.elegans]//0.019:72:81//Hs.5268:W22670
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:
 45 607:96//Hs.159273:AF054177
 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.
 152936:D63475
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910
 50 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24889:R49291
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190
 F-NT2RP2000173
 F-NT2RP2000175
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//
 55 Hs.100058:AB006713
 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
 F-NT2RP2000208

- F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:
243:61/Hs.143641:AB009462
- F-NT2RP2000232//EST/0.0087:187:62//Hs.151024:Z39990
- F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669
- F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378
- F-NT2RP2000248//EST/0.49:117:70//Hs.61016:AA019719
- F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)/0.51:227:60//Hs.30223:X90846
- F-NT2RP2000258//ESTs/3.1e-48:261:94//Hs.128230:AA972691
- F-NT2RP2000270//ESTs/2.9e-38:357:75//Hs.140329:AA714011
- F-NT2RP2000274//ESTs/1.1e-106:508:98//Hs.47646:AA307599
- F-NT2RP2000283//EST/1.0:139:63//Hs.128256:AA972910
- F-NT2RP2000288
- F-NT2RP2000289
- F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.
37138:U35376
- F-NT2RP2000298//ESTs/6.1e-46:322:85//Hs.159490:AI123467
- F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:
80//Hs.58218:UB2831
- F-NT2RP2000327//ESTs/4.3e-18:108:98//Hs.126212:AI417006
- F-NT2RP2000328//ESTs/6.3e-88:437:96//Hs.127336:AI332905
- F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:
X60673
- F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547
- F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:
97//Hs.76556:UB3981
- F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530
- F-NT2RP2000412//ESTs/1.0:214:60//Hs.91226:AA649047
- F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010
- F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]/3.9e-75:413:92//Hs.36779:
AA626790
- F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:
96//Hs.5819:AF102265
- F-NT2RP2000438//ESTs/1.3e-05:50:98//Hs.156532:AA913381
- F-NT2RP2000448//EST/1.1e-24:136:98//Hs.160402:AI393918
- F-NT2RP2000459//H.sapiens mRNA for imogen 38/1.9e-22:158:87//Hs.154655:Z68747
- F-NT2RP2000498//ESTs/1.0e-17:181:79//Hs.155243:N70293
- F-NT2RP2000503//ESTs/4.5e-41:205:100//Hs.62751:AA765702
- F-NT2RP2000510
- F-NT2RP2000516
- F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B mRNA EDITING PROTEIN [Rattus norvegicus]
//3.2e-15:167:75//Hs.10984:AA806768
- F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144
- F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)/1.0:
242:57//Hs.114001:Z20656
- F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514
- F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174
- F-NT2RP2000656
- F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602
- F-NT2RP2000668
- F-NT2RP2000678//ESTs/2.9e-16:310:65//Hs.126867:AI093453
- F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN
CHROMOSOME II PRECURSOR [Caenorhabditis elegans]/2.4e-31:233:78//Hs.114905:AA088442
- F-NT2RP2000710
- F-NT2RP2000715
- F-NT2RP2000731
- F-NT2RP2000758//EST/1.0e-14:199:71//Hs.162409:AA573242
- F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:
445:89//Hs.21421:AA911739

F-NT2RP2000809//ESTs/1.2e-36:235.89//Hs.154580:N34101
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds/0.22:351:58//Hs.159275:AF030880
 F-NT2RP2000814
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds/1.0:311:61//Hs.118087:AB011182
 5 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds/3.4e-28:390:70//Hs.20695:AB002292
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds/9.5e-29:167.94//Hs.
 75794:U80811
 F-NT2RP2000845//ESTs/1.0e-83:403.98//Hs.156828:AI336850
 10 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I
 [Schizosaccharomyces pombe]/6.4e-34:207.92//Hs.135253:AI081880
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:
 AB018284
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189.65//
 15 Hs.46146:AA418097
 F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from p21//5.5e-66:326:97//Hs.15144:AC005014
 F-NT2RP2000938//ESTs/1.8e-28:296.75//Hs.22822:H06408
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533.98//Hs.19822:
 20 AB018298
 F-NT2RP2000965//ESTs/5.3e-59:328:94//Hs.35575:R96494
 F-NT2RP2000970
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC
 25 REGION [Saccharomyces cerevisiae]//7.3e-76:385.96//Hs.21875:AA243700
 F-NT2RP2000987//ESTs/5.6e-11:177.72//Hs.15776:T91944
 F-NT2RP2001036//ESTs/2.0e-55:352.88//Hs.122131:AA789292
 F-NT2RP2001044//EST/0.069:267.60//Hs.102808:N67117
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.
 67619:AB007957
 30 F-NT2RP2001065
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds/1.0:310:60//Hs.3989:AB002313
 F-NT2RP2001081
 F-NT2RP2001094//ESTs/0.0071:262:64//Hs.128115:AI356560
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219
 35 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds/3.5e-33:519:63//Hs.80358:U52191
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]/6.4e-34:
 201:91//Hs.118470:AI336362
 F-NT2RP2001149//EST/3.9e-27:244:78//Hs.162236:AA551582
 F-NT2RP2001168//ESTs/0.0023:216:62//Hs.134938:AI091361
 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567.96//Hs.26247:
 AB007949
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011
 F-NT2RP2001196
 F-NT2RP2001218//ESTs/1.1e-65:337.96//Hs.115710:AA524598
 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053
 F-NT2RP2001233//Zinc finger protein 136 (clone pH-Z-20)/4.4e-58:656:70//Hs.69740:U09367
 F-NT2RP2001245//EST/0.018:228:62//Hs.116798:AA633813
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353
 F-NT2RP2001277//EST//0.42:127.66//Hs.42834:N20277
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412
 F-NT2RP2001295//ESTs/3.4e-29:90:100//Hs.123321:AA810287
 F-NT2RP2001312//ESTs/1.0:121:61//Hs.160261:AI146387
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359.71//Hs.76090:M80783
 F-NT2RP2001328//ESTs/5.2e-103:532:94//Hs.69476:AA628522
 55 F-NT2RP2001347//ESTs/4.3e-28:217:82//Hs.31775:H41883
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244
 F-NT2RP2001378
 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558

F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:
225:62/Hs.159402:AC005609

F-NT2RP2001394//ESTs/8.3e-22:133:78//Hs.109655:AI189767

F-NT2RP2001397//ESTs/0.090:265:60//Hs.152775:AA633088

5 F-NT2RP2001420
F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018
F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875

F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966

F-NT2RP2001440//Tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, eta polypeptide//
10 9.8e-56:603:72//Hs.75544:Z82248

F-NT2RP2001445//ESTs/2.2e-26:193:86//Hs.128610:AA504218

F-NT2RP2001449

F-NT2RP2001450

F-NT2RP2001467

15 F-NT2RP2001506
F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:
Y14494

F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134

20 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//
5.2e-105:384:94//Hs.99742:AF035586

F-NT2RP2001560
F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.
67619:AB007957

25 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389

F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876

F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:
AB018340

30 F-NT2RP2001613
F-NT2RP2001628//ESTs/4.9e-45:238:96//Hs.135222:AI082229

F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//
Hs.58488:U97067

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-
35 NA, complete cds//1.3e-145:687:97//Hs.159558:AF058718

F-NT2RP2001663//Enolase 1, (alpha)/4.2e-38:372:74//Hs.675:M14328

F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936

F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314

F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621 :
40 U52840

F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091

F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:
AI197870

F-NT2RP2001721

45 F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991

F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransf-
erase, geranyltransferase)//1.2e-19:151:86//Hs.77393:D14697

F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete_cds//5.2e-34:191:96//Hs.47504:
AF091754

50 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180

F-NT2RP2001839//EST//2.5e-12:86:94//Hs.132226:AI052250

F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610

F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete_cds//0.0013:174:62//Hs.9443:
AF027219

55 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768

F-NT2RP2001883

F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:
90//Hs.142189:M74161

F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
 F-NT2RP2001907//ESTs. Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754
 F-NT2RP2001936
 5 F-NT2RP2001943
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
 F-NT2RP2001947
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892
 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB01117
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299
 15 F-NT2RP2002032
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AJ003543
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198
 20 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:
 66//Hs.44553:AF055634
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183
 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
 F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156
 F-NT2RP2002089//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:
 AJ007509
 F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.
 30 122755:AF032986
 F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363
 F-NT2RP2002154//Homo sapiens mRNA for C1orf1 protein//1.0:149:65//Hs.100217:AJ008112
 F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314
 35 F-NT2RP2002185//ESTs. Weakly similar to ubiquitin S6 (1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:
 C06057
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Scl) mRNA, complete cds//3.7e-37:194:97//Hs.91728:
 M58460
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//
 40 6.8e-15:228:67//Hs.111323:AF077954
 F-NT2RP2002208
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318
 F-NT2RP2002239//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439
 45 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595:
 AF005418
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720
 F-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373
 50 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.
 24812:AF069532
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:
 55 95//Hs.31034:AB015594
 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637
 F-NT2RP2002373
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

97//Hs.109051:AF038958
 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16.456.59//Hs.90798.U79289
 F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069.265.65//Hs.74095.L20433
 F-NT2RP2002426//EST//4.3e-33.271.79//Hs.145743:AI269098
 5 F-NT2RP2002439//ESTs//0.00141.129.68//Hs.146064:AA714326
 F-NT2RP2002442//ESTs. Weakly similar to similar to molybdopterin biosynthesis MOEB proteins [C.elegans]//5.6e-
 26.169.89//Hs.25198:AA904265
 F-NT2RP2002457//ESTs//0.00031.121.71//Hs.134860:AI091436
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013.207.63//Hs.1560:D42045
 10 F-NT2RP2002475//ESTs//1.0.85.75//Hs.155371:AI139929
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125.607.96//Hs.
 125856:AB005289
 F-NT2RP2002498
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89.314.87//Hs.102681:U95044
 15 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159.761.97//Hs.23255:
 AB018334
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99.216.59//Hs.107563:M28212
 F-NT2RP2002537
 F-NT2RP2002546//EST//0.81.161.65//Hs.120562:AA741096
 20 F-NT2RP2002549//ESTs//0.76.228.61//Hs.146313:AA594979
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33.285.78//Hs.159277:
 AB018341
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39.377.59//Hs.2522.Z35309
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24.144.95//Hs.23094:M19503
 25 F-NT2RP2002609//Human guanine nucleotide regulatory protein (GDPBP1) mRNA, complete cds//1.0.120.68//Hs.334:
 U02082
 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28.460.63//Hs.
 20521:Y10805
 F-NT2RP2002621
 30 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022.210.64//Hs.
 155302:U57317
 F-NT2RP2002672//ESTs//7.4e-30.226.84//Hs.94694:WS2493
 F-NT2RP2002701//ESTs. Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
 [Caenorhabditis elegans]//8.3e-56.278.97//Hs.109857:AA088385
 35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042.367.61//Hs.662:M58583
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42.631.65//Hs.6336:
 AB014572
 F-NT2RP2002727
 F-NT2RP2002736//ESTs//3.2e-67.336.97//Hs.86583:AA761217
 40 F-NT2RP2002740//EST//1.0e-70.352.97//Hs.145168:AI150297
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30.628.62//Hs.87435:D89016
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29.285.75//Hs.146395:AB002329
 F-NT2RP2002752//EST//2.2e-06.126.74//Hs.159913:AA862709
 F-NT2RP2002753//ESTs//4.3e-14.137.81//Hs.133478:T77905
 45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017.507.57//Hs.79706:U53204
 F-NT2RP2002778//EST//1.6e-57.319.93//Hs.147519:AI216407
 F-NT2RP2002800
 F-NT2RP2002839//ESTs//0.075.177.62//Hs.132445:AA921763
 F-NT2RP2002857//ESTs//0.99.88.69//Hs.132104:AI382142
 50 F-NT2RP2002862
 F-NT2RP2002880
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0.237.62//Hs.106487:AB014573
 F-NT2RP2002925//ESTs//1.6e-33.318.77//Hs.16808:W22606
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136.623.99//Hs.
 116674:AF038392
 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24.158.65//Hs.108447:AJ000517
 F-NT2RP2002939
 F-NT2RP2002954

F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21:
135.91//Hs.108332;U39317
F-NT2RP2002979
F-NT2RP2002980
5 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.
122967;AF059569
F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965;AI004740
F-NT2RP2002993
F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464;AF088219
10 F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048;AA10971
F-NT2RP2003073//Human clone 230971 definitive mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:
78//Hs.159176;U92019
F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276;L09190
F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704;U11050
15 F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408;AA416633
F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998;AI291379
F-NT2RP2003125//Serum response factor (fos serum response element-binding transcription factor)//4.5e-06:
556.57//Hs.155321;J03161
F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836;AA121544
20 F-NT2RP2003137
F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958;AB014520
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:
D67025
F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532;AI424170
25 F-NT2RP2003164//EST//0.11:179:63//Hs.163299;AA853944
F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014;AB002353
F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767;N91123
F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531;AI393223
F-NT2RP2003206//EST//0.095:182:60//Hs.88461;AA278594
30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443;X74794
F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720;AA526947
F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA, com-
plete cds//1.3e-62:543:77//Hs.108966;U48696
F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:
35 200:62//Hs.102732;U881513
F-NT2RP2003265
F-NT2RP2003272//ESTs. Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:
C06057
40 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:
AB014525
F-NT2RP2003280
F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:
AB011159
F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227;AI269334
45 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.
7943;AB006572
F-NT2RP2003297//EST//0.99:240:60//Hs.133228;AI052312
F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020;AA442752
F-NT2RP2003308
50 F-NT2RP2003329//ESTs. Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III
[Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092;T75227
F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649;AI346765
F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003;H85963
F-NT2RP2003367//Human HsLim15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108
55 F-NT2RP2003391
F-NT2RP2003393
F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976;AF039023
F-NT2RP2003401

- F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/3.7e-33.303.77//Hs.14038:R06800
- F-NT2RP2003445//EST//1.7e-06.154.65//Hs.142843:R36893
- F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273.61//Hs.159360:L22647
- 5 F-NT2RP2003456//EST//0.17.95.65//Hs.147190:AI193320
- F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53.339.78//Hs.132874.AC004770
- F-NT2RP2003480//Calpain, small polypeptide//1.1e-06.154.66//Hs.74451:X04106
- F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10.481.60//Hs.80220:U96136
- 10 F-NT2RP2003506
- F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76.189.62//Hs.107164:M96803
- F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78.403.94//Hs.78482:Y16270
- F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)/1.3e-24.151.95//Hs.1976:M12783
- 15 F-NT2RP2003522//Zinc finger protein 148 (PHZ-52)//1.1e-17.512.60//Hs.112180:AF039019
- F-NT2RP2003533//ESTs//1.8e-76.373.98//Hs.140402:AI138765
- F-NT2RP2003543//ESTs//9.3e-65.363.92//Hs.70643:AA030010
- F-NT2RP2003559//ESTs//0.00037.93.77//Hs.157564:AI356513
- F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28.664:
- 20 63//Hs.1042:M62800
- F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114.541.98//Hs.129937:AB007931
- F-NT2RP2003581//EST//1.0:59.76//Hs.158575:AI368947
- F-NT2RP2003586//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63.224.95//Hs.34627:
- 25 AA126463
- F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124.585.98//Hs.58488:U97067
- F-NT2RP2003629//ESTs//2.0e-103.535.95//Hs.105633:AA479166
- F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85.216.61//Hs.89591:M97252
- 30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47.371.80//Hs.125231:AF068006
- F-NT2RP2003687//EST//2.9e-14.134.80//Hs.132635:AI032875
- F-NT2RP2003691//ESTs//8.2e-47.296.83//Hs.138852:AA284247
- F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85.190.61//Hs.18366:L09561
- 35 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44.269.91//Hs.139757:N95271
- F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110.518.98//Hs.78494:AB011097
- F-NT2RP2003713
- F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:
- 40 252.83//Hs.86371:AF054180
- F-NT2RP2003727//EST//0.52.277.59//Hs.69507:AA111879
- F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:
- 584.71//Hs.118797:U39318
- F-NT2RP2003751
- 45 F-NT2RP2003760
- F-NT2RP2003764
- F-NT2RP2003769
- F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58.247.59//Hs.96055:U47677
- F-NT2RP2003777
- 50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63.356.92//Hs.16131:AA568689
- F-NT2RP2003793//ESTs//4.8e-68.392.92//Hs.93949:AA782955
- F-NT2RP2003825//ESTs//7.6e-79.232.98//Hs.14347:AA287742
- F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95.300.59//Hs.77768:X63368
- F-NT2RP2003857//EST//1.0.112.62//Hs.139216:AA244425
- 55 F-NT2RP2003859
- F-NT2RP2003871//ESTs//2.5e-44.222.99//Hs.146295:AA935780
- F-NT2RP2003885
- F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emerichella nidulans]//2.2e-

113.632.92//Hs.50072:AI378221
F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.
156920:AA489296
F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.
5 35086:AB014458
F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:
AB007916
F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347
F-NT2RP2003984
10 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036
F-NT2RP2003988//thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//
Hs.111081:AI380378
F-NT2RP2004014
15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
F-NT2RP2004042
F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:
AF011573
F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942
20 F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:
60//Hs.104315:AF054826
F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
F-NT2RP2004142
F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
25 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966
F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501
F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:
AA626790
30 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:
U57317
F-NT2RP2004196
F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
F-NT2RP2004226//ESTs, Weakly Similar to leg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270
35 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:
40 N25951
F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263
F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:
157:67//Hs.37121:Z37544
F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:
45 AF00416
F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
50 F-NT2RP2004365
F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:
AF000986
F-NT2RP2004373
F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III
55 [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916
F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164
F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468

F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367
 F-NT2RP2004412
 F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944
 F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687
 5 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//0.45:
 208:61/Hs.24040:AF006823
 F-NT2RP2004490
 F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203
 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//
 10 Hs.73614:U83460
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:
 AB011163
 F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891
 F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:
 15 AF039694
 F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219
 F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309
 F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898
 F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895
 20 F-NT2RP2004602//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.0e-59:
 273:93//Hs.12845:N28835
 F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:
 25 AB007929
 F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839
 F-NT2RP2004681
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:
 AB014525
 30 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942
 F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:
 AB007947
 F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242
 35 F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183
 F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//
 3.7e-110:548:96//Hs.85768:W16504
 F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.
 107474:AF045451
 40 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:
 L40157
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
 4.9e-118:594:95//Hs.40820:AF058953
 F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043
 45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:
 AF054179
 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161
 F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258
 F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111
 50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144
 F-NT2RP2004936
 F-NT2RP2004959
 F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763
 F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478
 55 F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735
 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927
 F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.
 41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478
 F-NT2RP2004999
 F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//
 Hs.124161:AF065164
 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:
 AB014515
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141
 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600
 10 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612
 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:
 15 AF055917
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA6857838
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:
 AB014564
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.
 20 100555:X98743
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:
 AF045583
 25 F-NT2RP2005147
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:63:96//Hs.155218:
 AJ007509
 30 F-NT2RP2005204//H.sapiens ST4 gene for ST4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.1292528:AA994783
 F-NT2RP2005245//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341
 35 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.
 81452:AF030555
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//
 Hs.27007:AF060219
 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:
 AB014576
 F-NT2RP2005325//Human LIM-homeobox domain protein (HLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.
 45 1569:U11701
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190KD subunit (SNAP190) mRNA, complete
 cds//0.016:353:62//Hs.113265:AF032387
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138
 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958
 50 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:
 489:96//Hs.107254:AC005943
 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122
 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.
 113252:U80761
 55 F-NT2RP2005407
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

- F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tauri]/[8.5e-48:295.90//Hs.75017:AA166853]
- F-NT2RP2005464//ESTs/[2.0e-99:495.96//Hs.3530:AA808243]
- F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog/[0.032:176.64//Hs.16:D10656]
- 5 F-NT2RP2005472//ESTs/[1.4e-34:180.98//Hs.158892:AD78412]
- F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds/[9.9e-48:432.77//Hs.15519:AB018315]
- F-NT2RP2005490//ESTs/[4.5e-19:165.84//Hs.134382:AA083573]
- F-NT2RP2005491
- 10 F-NT2RP2005495//ESTs/[5.6e-96:452.99//Hs.145417:AI084164]
- F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds/[4.4e-48:621.68//Hs.6833:AB002324]
- F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds/[1.6e-63:503.78//Hs.7688:M64930]
- F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds/[0.56:139.66//Hs.8546:U97669]
- 15 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//[1.0:291.59//Hs.89709:L35546]
- F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds/[1.2e-82:44.92//Hs.119023:AF092563]
- F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds/[2.2e-19:112.99//Hs.6232:AB018307]
- 20 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]/[3.5e-50:366.83//Hs.61833:AA036735]
- F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)/[9.4e-155:747.97//Hs.159597:AJ012449]
- 25 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds/[1.9e-131:618.98//Hs.62515:AB007963]
- F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III [C.elegans]/[2.5e-51:292.93//Hs.105684:H24407]
- F-NT2RP2005555//EST/[0.046:308.57//Hs.145962:AI276822]
- 30 F-NT2RP2005557//ESTs/[4.6e-48:382.79//Hs.125014:AI242289]
- F-NT2RP2005561//ESTs/[6.3e-28:166.93//Hs.87803:AA034436]
- F-NT2RP2005600//ESTs/[1.6e-04:228.93//Hs.160085:AI218627]
- F-NT2RP2005605//ESTs/[5.7e-13:115.86//Hs.37718:H60071]
- F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds/[3.1e-92:447.97//Hs.22396:AF062085]
- 35 F-NT2RP2005622//ESTs/[0.16:242.63//Hs.16395:AA523702]
- F-NT2RP2005635
- F-NT2RP2005637//ESTs/[0.055:96.69//Hs.105998:R90905]
- F-NT2RP2005640//ESTs/[4.5e-16:107.92//Hs.150823:AI292145]
- F-NT2RP2005645//ESTs/[2.7e-29:181.90//Hs.121653:AI375440]
- 40 F-NT2RP2005651//Oxysterol binding protein/[0.00011:122.69//Hs.1433065:M86917]
- F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds/[1.5e-08:351.62//Hs.91400:AB006626]
- F-NT2RP2005669//ESTs/[0.016:185.64//Hs.97713:AA442239]
- 45 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds/[7.7e-96:462.98//Hs.25664:AF089814]
- F-NT2RP2005683//ESTs/[0.83:242.62//Hs.136395:AA523702]
- F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE/[2.5e-11:328.61//Hs.79217:M77836]
- F-NT2RP2005694
- F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds/[0.15:496:55//Hs.79326:L76703]
- F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds/[5.1e-126:599.97//Hs.61638:AB018342]
- F-NT2RP2005719//ESTs/[0.58:326.60//Hs.157209:N57527]
- F-NT2RP2005722//Cinc finger protein 136 (clone pH-Z-20)/[8.2e-46:415.77//Hs.69740:U09367]
- 55 F-NT2RP2005723//ESTs/[1.0e-15:141.81//Hs.163747:AA174017]
- F-NT2RP2005726//EST/[3.4e-15:96.95//Hs.156170:AI334191]
- F-NT2RP2005732//ESTs/[0.99:162.62//Hs.154914:AA721086]
- F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and/[0.80:362.58//Hs.97220:U96769]

F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X686688
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//
 Hs.159651:AF068888
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.
 5 26285:AF082516
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853
 F-NT2RP2005767//Homolog 2 of Drosophila large discs/0.085:262:61//Hs.23205:X62895
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836
 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:
 10 Z50115
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.
 34853:U28368
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820
 15 F-NT2RP2005812
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595
 F-NT2RP2005835
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//
 Hs.59829:AB014602
 20 F-NT2RP2005853
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:
 98//Hs.50758:AF092564
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567
 F-NT2RP2005868
 25 F-NT2RP2005866//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:
 L16782
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399
 30 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:
 AA292186
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339
 F-NT2RP2006023
 35 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416
 40 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970
 F-NT2RP2006100
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240
 45 F-NT2RP2006166
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:
 AB014554
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:
 50 AB018315
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503
 F-NT2RP2006219//H.sapiens mRNA for DGC6 protein//4.4e-118:618:93//Hs.153910:X96484
 F-NT2RP2006237
 F-NT2RP2006238
 55 F-NT2RP2006258//ESTs//0.0034:143:89//Hs.145798:AI269970
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:
 60//Hs.75111:D87258

- F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262
 F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-29:151:100//Hs.
 36794:AI038407
 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371
 5 F-NT2RP2006323//Homo sapiens mRNA for NBPbox, complete cds//4.7e-06:170:70//Hs.87202:D82344
 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:
 AF076974
 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174
 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501
 10 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA20341
 F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.
 95838:AF059734
 F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934
 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509
 15 F-NT2RP2006456
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs.72160:AJ006266
 F-NT2RP2006467
 F-NT2RP2006472
 F-NT2RP2006476
 F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
 20 F-NT2RP2006554//EST//0.80:116:65//Hs.160110:AA922134
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete
 cds//2.1e-115:669:90//Hs.31218:AF038966
 F-NT2RP2006571//Cytochrome P450, subfamily IIa (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.
 73864:U22029
 25 F-NT2RP2006573
 F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
 F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:
 AJ011972
 30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:
 AF000560
 F-NT2RP3000047
 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.
 37138:U35376
 35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961
 F-NT2RP3000068
 F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
 F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670
 F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608
 40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140
 F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:
 AB011164
 45 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503
 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.
 127338:AB007961
 F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779
 F-NT2RP3000207
 50 F-NT2RP3000220
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.
 122967:AF059569
 F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972
 55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
 F-NT2RP3000252
 F-NT2RP3000255
 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.
80261:L43821

F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863

F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//
0.0088:236:63//Hs.102732:AA88153

F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242

F-NT2RP3000331//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]/0.57:189:65//
Hs.46146:AA418097

F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390

F-NT2RP3000348

F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754

F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:
X60673

F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921

F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]/4.0e-116:
596:95//Hs.21094:AI337016

F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639

F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:
AF071185

F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503

F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948

F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487

F-NT2RP3000441

F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562

F-NT2RP3000451//Receptor protein-tyrosine kinase EDR1//0.95:315:58//Hs.75562:U48705

F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068

F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822

F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058

F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667

F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379

F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966

F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308

F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412

F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404

F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723

F-NT2RP3000578

F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277

F-NT2RP3000584

F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904

F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914

F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.117841:AA179811

F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]/9.3e-61:355:92//Hs.114622:AA693492

F-NT2RP3000603//Human mRNA for KIAA227 gene, partial cds//6.3e-10:553:59//Hs.79170:D66980

F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.1217152:AI421203

F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683

F-NT2RP3000624//6A KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162

F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333

F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904

F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219

F-NT2RP3000661

F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.
13063:AF017789

F-NT2RP3000685

F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001

F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884

F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854

F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

F-NT2RP3000753//ESTs//2.6e-63:318.97//Hs.153000:AA777785
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245.91//Hs.
 2427:D89937
 F-NT2RP3000815
 5 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132
 F-NT2RP3000826//Homo sapiens deltaex (Dx) mRNA, complete cds//0.00040:263.65//Hs.124024:AF053700
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapi-
 ens]//1.e-71:363.96//Hs.23803:AA126476
 F-NT2RP3000841//EST//1.36:224.60//Hs.162094:AA524012
 10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593.68//Hs.157199:
 X97630
 F-NT2RP3000847//ESTs//0.0028:56.92//Hs.116406:AA209520
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323.86//Hs.155464:AF088219
 F-NT2RP3000852
 15 F-NT2RP3000859//ESTs//0.39:169.62//Hs.148948:AA699918
 F-NT2RP3000865//EST//0.15:236.62//Hs.123366:AA811476
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds//6.4e-31:766.60//Hs.15432:U53445
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.e-13:701.60//Hs.79706:U53204
 20 F-NT2RP3000875
 F-NT2RP3000901//ESTs//8.2e-26:191.87//Hs.18793:R99101
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374
 F-NT2RP3000917
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340.60//Hs.109895:X68277
 25 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351.83//Hs.2953:X84407
 F-NT2RP3000980//ESTs//6.5e-10:102.81//Hs.86950:AI204212
 F-NT2RP3000994//ESTs//4.1e-120:571.98//Hs.127295:AA918411
 F-NT2RP3001004//ESTs//1.e-76:438.88//Hs.144554:N92198
 F-NT2RP3001007
 30 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//
 2.9e-12:1:588.98//Hs.128781:AA160707
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282.97//Hs.
 30303:AI244662
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534.74//
 35 Hs.27007:AF060219
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474.60//Hs.21264:AB018325
 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP) //4.4e-16:428.60//Hs.155481:
 AJ006470
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712.64//Hs.82292:D86969
 40 F-NT2RP3001109//ESTs//1.2e-67:323.99//Hs.134734:AI337050
 F-NT2RP3001111
 F-NT2RP3001113//EST//1.1e-33:173.99//Hs.112640:AA609088
 F-NT2RP3001115//EST//1.3e-22:122.100//Hs.162990:AA688023
 F-NT2RP3001116//ESTs//1.1e-15:93.98//Hs.58412:W74779
 45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258.61//Hs.12107:AF042384
 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20) //2.4e-77:687.75//Hs.69740:U09367
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341.60//Hs.94790:
 AB018318
 F-NT2RP3001133//Homeo box A4//0.00011:484.59//Hs.77637:M74297
 50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851.98//Hs.5378:AB018305
 F-NT2RP3001147
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257.59//Hs.957:M84605
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891.98//Hs.72160:AJ006266
 F-NT2RP3001176
 55 F-NT2RP3001214//EST//0.88:218.60//Hs.161147:AI417859
 F-NT2RP3001216//ESTs//1.5e-66:340.96//Hs.105994:W19981
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512.95//Hs.103816:AA130866
 F-NT2RP3001232//EST//0.0016:116.71//Hs.136498:AA594010

F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132
 F-NT2RP3001253//Human prepromelittin mRNA, complete cds//0.99:293:60//Hs.32934:U27109
 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:
 AB018269
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:
 72//Hs.41728:L75847
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566
 10 F-NT2RP3001274
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:
 U44060
 15 F-NT2RP3001318//Amylase, 1,6-glucosidase, 4-alpha-glucantransferase (glycogen debranching enzyme, glycogen storage disease type III)/0.012:52:56//Hs.904:U84010
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:
 20 AB007920
 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (I_H1) mRNA, partial cds//0.00019:473:
 61//Hs.124161:AF065164
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//
 1.1e-81:421:96//Hs.32508:H29831
 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487
 F-NT2RP3001374//ESTs//0.98:289:59//Hs.125303:AA873022
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451
 F-NT2RP3001384//Homo sapiens mRNA for HRHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595
 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:
 66//Hs.41728:L75847
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.
 111024:L77567
 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047
 F-NT2RP3001426
 F-NT2RP3001427
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type I//1.8e-73:431:91//Hs.85844:X66397
 40 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.e-
 05:195:65//Hs.115868:AA568393
 F-NT2RP3001447
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212
 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323
 F-NT2RP3001459
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:
 AF072836
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877
 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//
 2.8e-172:804:98//Hs.28285:AF064801
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:
 91//Hs.85283:U36500
 55 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.
 105912:A1431328
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2/1.9e-06:426:59//Hs.162:X16302
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)/0.049:185:65//Hs.1686:
 M69013
 F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/9.6e-51:345:82//Hs.144563:
 5 AF057280
 F-NT2RP3001607//ESTs/1.3e-07:299:63//Hs.43231:N22688
 F-NT2RP3001608//ESTs/5.7e-14:85:98//Hs.161133:AI091349
 F-NT2RP3001621//ESTs/1.6e-106:310:96//Hs.128505:AA306435
 F-NT2RP3001629
 10 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149
 F-NT2RP3001642//ESTs/1.0:148:63//Hs.159495:T70173
 F-NT2RP3001646
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)/1.1e-172:816:98//Hs.159597:
 AJ012449
 15 F-NT2RP3001672//ESTs/5.0e-16:138:82//Hs.151864:T69027
 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]/9.0e-53:
 375:85//Hs.41127:AA555184
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZX757.1 IN CHROMOSOME III
 20 [Caenorhabditis elegans]/4.0e-11:518:99//Hs.20364:AI420022
 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198
 F-NT2RP3001690//EST/0.15:291:59//Hs.162336:AA564329
 F-NT2RP3001698//ESTs/0.24:134:69//Hs.129551:AA885219
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [D.mela-
 25 nogaster]/1.4e-31:191:94//Hs.131279:AA486291
 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
 //7.6e-159:747:98//Hs.6823:W18181
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:
 30 565:97//Hs.159273:AF054177
 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III
 [Caenorhabditis elegans]/3.5e-116:554:98//Hs.144332:AA046836
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918
 F-NT2RP3001739
 35 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete
 cds//0.10:528:56//Hs.22138:U49250
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:
 U27193
 40 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.
 57783:U78525
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:
 AB007928
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532
 45 F-NT2RP3001799//ESTs/0.0088:178:64//Hs.134938:AI091361
 F-NT2RP3001819//Collagen, type IX, alpha 3/0.026:530:58//Hs.53563:L41162
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634
 F-NT2RP3001854//ESTs/1.5e-100:501:96//Hs.72217:AA166729
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:
 50 U68727
 F-NT2RP3001857//ESTs/2.7e-85:414:98//Hs.151001:AA564706
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans]/2.9e-94:452:98//Hs.54952:
 AA872675
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326
 55 F-NT2RP3001915//ESTs/1.1e-83:397:99//Hs.151725:AA723896
 F-NT2RP3001926//EST/0.53:362:57//Hs.127917:AA969185
 F-NT2RP3001929//ESTs/7.4e-16:141:82//Hs.138852:AA284247
 F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)/0.0022:268:61//Hs.106070:U22398
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:
 AB014575
 F-NT2RP3001944//ESTs/0.00052:60:91//Hs.131731:AI339335
 5 F-NT2RP3001969
 F-NT2RP3001989//EST/0.00016:263:63//Hs.144096:AI032180
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)/4.0e-61:293:83//Hs.155464:AF088219
 F-NT2RP3002004//H.sapiens mRNA for FAST kinase/5.2e-28:104:100//Hs.75087:X86779
 F-NT2RP3002007//ESTs/0.025:88:69//Hs.163310:AA856946
 10 F-NT2RP3002014//ESTs/4.8e-70:291:98//Hs.123693:AA238321
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]/3.8e-48:353:81//Hs.127507:
 AA993745
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]/3.0e-25:212:83//Hs.71622:AA195155
 15 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]/4.2e-82:
 407:97//Hs.131888:AI091806
 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames/3.7e-21:168:85//Hs.23094:M19503
 F-NT2RP3002062//EST/0.46:198:62//Hs.157711:AI359710
 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)/
 20 0.91:194:65//Hs.1298.J03779
 F-NT2RP3002081
 F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:
 297:61//Hs.102732:U88153
 F-NT2RP3002102//EST/2.8e-16:237:67//Hs.136255:T70256
 25 F-NT2RP3002108
 F-NT2RP3002142//ESTs/4.3e-138:654:98//Hs.5729:AA306018
 F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1/0.27:276:62//Hs.5923:X82260
 F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with
 some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative
 30 CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009
 F-NT2RP3002151//G1 to S phase transition/1/2.6e-37:292:81//Hs.2707:X17644
 F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985
 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]
 35 //3.0e-61:340:93//Hs.11379:AA594140
 F-NT2RP3002166//EST/0.039:114:69//Hs.140335:AA737046
 F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME
 III [Caenorhabditis elegans]/4.0e-39:255:72//Hs.141429:AA631915
 F-NT2RP3002181//ESTs/3.6e-111:518:99//Hs.128505:AA30643
 F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)/0.98:
 40 242:57//Hs.114001:Z20656
 F-NT2RP3002248
 F-NT2RP3002255//ESTs/8.4e-19:227:75//Hs.122817:AA772261
 F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.
 110637:AC004080
 45 F-NT2RP3002276//ESTs/8.2e-97:463:98//Hs.45120:AA225139
 F-NT2RP3002303//ESTs/7.1e-10:96:87//Hs.135700:AA989386
 F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910
 F-NT2RP3002330//ESTs/1.3e-81:482:90//Hs.121460:AA744871
 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383
 50 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE/1.6e-65:
 588:75//Hs.154672:X16396
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:
 Y16355
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200
 55 F-NT2RP3002399
 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]/4.3e-41:233:94//Hs.22880:AA056274
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:
 AB014578

F-NT2RP3002484//ESTs/0.95:166:63//Hs.149993:AI291310
 F-NT2RP3002501//ESTs/0.92:43:90//Hs.119314:AA432108
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.
 5 57738:U35246
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:
 AB018272
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.
 96759:AA469984
 10 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706
 F-NT2RP3002587//EST/4.8e-31:330:74//Hs.139415:AA426054
 F-NT2RP3002590//EST/1.3e-40:202:100//Hs.144716:AI187919
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508
 F-NT2RP3002603
 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:
 AJ006470
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.
 20 151518:U38847
 F-NT2RP3002660//ESTs/2.9e-32:164:100//Hs.152982:AA584308
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//
 Hs.41086:AI337400
 F-NT2RP3002671//ESTs/3.7e-05:288:59//Hs.161359:AI241991
 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584
 F-NT2RP3002687
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657
 F-NT2RP3002713//ESTs/0.93:229:61//Hs.150459:AI279514
 30 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//
 Hs.129736:AF040753
 F-NT2RP3002785
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713
 35 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:
 AF004715
 F-NT2RP3002861//ESTs/1.1e-88:468:94//Hs.158821:AA524070
 F-NT2RP3002869//ESTs/3.4e-23:132:97//Hs.148873:T33582
 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895
 F-NT2RP3002877//ESTs/1.1e-19:160:84//Hs.118273:AA626040
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//
 45 Hs.3826:U69560
 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:
 AB011160
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
 50 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703
 F-NT2RP3002985//Human TFIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:
 U28838
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308
 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083
 F-NT2RP3003032//ESTs/9.1e-40:241:92//Hs.113636:C06446
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
 F-NT2RP3003078
 F-NT2RP3003101
 5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:
 88:68//Hs.99715:AA292700
 F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740
 F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1)
 mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
 10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
 F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:
 63//Hs.118397:AF053944
 F-NT2RP3003150
 F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.
 15 37138:U35376
 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
 F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933
 F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
 F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
 20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
 F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
 F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
 F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:
 D44497
 25 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:
 AF055460
 F-NT2RP3003251//H.sapiens Staf50 mRNA//1.e-68:651:76//Hs.68054:X82200
 F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//
 Hs.620:M69225
 30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:
 AF04924
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953
 F-NT2RP3003301//EST//1.0e-58:74//Hs.158575:AI368947
 35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058
 F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200
 F-NT2RP3003330
 40 F-NT2RP3003344
 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542
 F-NT2RP3003384//ESTs//1.1e-65:346:98//Hs.35012:R92791
 45 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:
 63//Hs.113272:U90653
 F-NT2RP3003411//Human metallothionein-1e gene (hMT-1e)//0.99:116:62//Hs.74170:M10942
 50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.
 14934:AF004828
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:
 55 AB018268
 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

AF038169
F-NT2RP3003552
F-NT2RP3003555//ESTs/1.4e-12:81:98//Hs.144487:AI418322
F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365
5 F-NT2RP3003572//EST/0.27:105:69//Hs.162134:AA526311
F-NT2RP3003576//ESTs/1.2e-57:277:84//Hs.138852:AA284247
F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741
F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:
D14012
10 F-NT2RP3003625
F-NT2RP3003656
F-NT2RP3003659
F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586
F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184
15 F-NT2RP3003680//Human Bcl2. p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:
63//Hs.44585:U58334
F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000
F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848
F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865
20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:
AB018300
F-NT2RP3003746
F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230
F-NT2RP3003799
25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:
M19722
F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:
242:57//Hs.114001:Z20656
F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//
30 5.1e-07:624:59//Hs.96028:AF042832
F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.
102877:U41315
F-NT2RP3003825
F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481
35 F-NT2RP3003831
F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:
AF070611
F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:MT3780
F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268
40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:
AB018343
F-NT2RP3003876//ESTs. Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576
F-NT2RP3003914//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE
45 PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659
F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:
404:77//Hs.9006:AF057358
F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396
F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006
F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.
50 93909:AF042498
F-NT2RP3004013//ESTs. Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.
142151:AA984061
F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.
155302:U57317
55 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234
F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317
F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875
F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.

100007:X76091
F-NT2RP3004093
F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258
F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390
5 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509
F-NT2RP3004145
F-NT2RP3004148
F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:
10 AF032900
F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706
F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:
62//Hs.101047:M31523
15 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835
F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361
F-NT2RP3004242
F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240
F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140
20 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067
F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.
158471:AF088982
F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871
F-NT2RP3004332
25 F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285
F-NT2RP3004341//EST//0.0068:213:64//Hs.153202:X98426
F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999
F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME
III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915
30 F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//
4.3e-125:608:98//Hs.128781:AA160707
F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122:
X97249
F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113
35 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403
F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2) //0.00023:357:59//Hs.99948:M97016
F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:
AB007917
F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564
40 F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219
F-NT2RP3004472
F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925
F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//
4.6e-118:547:99//Hs.124768:AA307735
45 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851
F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [Mus musculus]//3.5e-89:425:99//Hs.126082:AI077718
F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256
F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948
F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046
50 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110
F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571
F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:
AB014532
F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:
55 AB011126
F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.
125870:AI364967
F-NT2RP3004569

- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97//
Hs.122752:AF026445
- F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:
AB007923
- 5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
- F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//
Hs.124138:AI266336
- F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA090232
- F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
- 10 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
- F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//
Hs.118991:AA675919
- F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668
- F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
- 15 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761
- F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:
AJ006470
- F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:
AJ012449
- 20 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
- F-NT2RP4000111
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:
AB007952
- 25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069
- F-NT2RP4000150
- F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
- F-NT2RP4000159
- F-NT2RP4000167
- 30 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
- F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:
AB014600
- F-NT2RP4000212//ESTs//1.1e-10:74:95//Hs.111885:AA422006
- F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
- 35 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.
46468:U45984
- F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:
AJ006470
- F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:
384:89//Hs.115498:AA436298
- 40 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:
AF091092
- F-NT2RP4000263
- F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
- 45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
- F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.
143648:AB000732
- F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
- F-NT2RP4000355
- 50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:
AB018281
- F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-
137:649:97//Hs.31323:AF044195
- F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECUR-
SOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073
- F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//
0.098:291:59//Hs.994:M95678
- F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

- F-NT2RP4000398/Zinc finger protein 140 (clone pHZ-39)/4..9e-60.469:63//Hs.154205:U09368
 F-NT2RP4000415//ESTs/0..85:89:67//Hs.152312:AA485688
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:
 AF027156
 5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:43:73//Hs.
 46468:U45984
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087
 F-NT2RP4000449//EST/0..84:113:65//Hs.145274:A1249468
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
 10 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HALUSP)//1.1e-05:
 532:57//Hs.78683:Z72495
 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535
 F-NT2RP4000481//Human mRNA for KIAA0286 gene, partial cds//0.46:272:58//Hs.78862:D87742
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.
 15 159234:U89995
 F-NT2RP4000500//myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
 F-NT2RP4000517//EST/0..043:131:64//Hs.99030:A0443904
 F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:
 20 AJ010840
 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372
 F-NT2RP4000524
 F-NT2RP4000528
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154
 25 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.
 25597:H93026
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA1778351
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.
 30 4214:AF067730
 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:
 60//Hs.144626:AF100907
 35 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.e-167:676:
 98//Hs.50748:AB004848
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, com-
 plete cds//6.9e-07:494:61//Hs.113286:U77783
 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622
 40 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178
 F-NT2RP4000737//Human mRNA for KIAA0256 gene, partial cds//0.97:409:60//Hs.83419:D87440
 F-NT2RP4000739//DESMOPLOAKIN I AND II//0.99:192:63//Hs.74316:AL031058
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
 45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:
 AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
 F-NT2RP4000839//ESTs//5..7e-11:133:82//Hs.103852:W27603
 50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROCI-1B) mRNA, complete cds//1.4e-37:680:63//Hs.
 75875:U49278
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803
 F-NT2RP4000879//ESTs//0..89:184:64//Hs.122333:AA782843
 55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901
 F-NT2RP4000918
 F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

- F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//
 Hs.24812:AF069532
 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371
 5 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058
 F-NT2RP4000979
 F-NT2RP4000984
 10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204
 F-NT2RP4001004
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718
 15 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.
 113287:AF009204
 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:
 L40157
 20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:
 AJ006470
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
 F-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial//1.4e-131:634:98//Hs.
 25 106778:AJ010953
 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) (alternative products)//0.025:166:66//Hs.
 146459:X66975
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164
 F-NT2RP4001095
 30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis
 familiaris]//2.e-26:171:92//Hs.14038:R06800
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:
 35 100//Hs.126925:AA931237
 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
 40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734
 F-NT2RP4001159//EST//0.26:125:66//Hs.1520292:AA377324
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324
 F-NT2RP4001207
 45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636
 F-NT2RP4001213//KRAB zinc finger protein (alternative products)//1.1e-45:187:74//Hs.22556:U37251
 F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.
 122967:AF059569
 50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778
 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463
 F-NT2RP4001260//Syntrphin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//
 Hs.31121:U40571
 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578
 55 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
 mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250
 F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

F-NT2RP4001336//ESTs/1.0:128:67//Hs.99598:AA603110
 F-NT2RP4001339
 F-NT2RP4001343
 5 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625
 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds//2.0e-31:784:62//Hs.15432:U53445
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356
 F-NT2RP4001372
 10 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194
 F-NT2RP4001375
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918
 F-NT2RP4001407//Homo sapiens mRNA for RG55, complete cds//0.93:218:58//Hs.24950:AB008109
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957
 15 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933
 F-NT2RP4001442
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:
 AB018326
 20 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.
 26676:AA033997
 F-NT2RP4001485//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523
 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.
 63220:AA522707
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395
 25 F-NT2RP4001507//H.sapiens mRNA for RangTPase activating protein 1//0.51:281:61//Hs.5923:X82260
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:
 U13220
 30 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534
 F-NT2RP4001555//EST//0.99:225:64//Hs.96363:AA347174
 F-NT2RP4001567
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC
 REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836
 35 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
 F-NT2RP4001574
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228
 F-NT2RP4001592
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
 40 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952
 F-NT2RP4001634
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC
 REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436
 45 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409
 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECUR-
 SOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:
 67//Hs.30250:AF055376
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080
 50 F-NT2RP4001696
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.
 92614:M62302
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
 55 F-NT2RP4001753//Zinc finger protein 84 (HPF2) //4.5e-29:476:67//Hs.9450:M27878
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:
 AC004522

F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
 F-NT2RP4001822//ESTs/3.4e-50:307:90//Hs.113509:AA132131
 F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:
 5 U11690
 F-NT2RP4001828
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
 F-NT2RP4001841//ESTs/0.99:215:60//Hs.136895:AA897749
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:
 10 AB014572
 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:
 84:94//Hs.140232:AA705170
 F-NT2RP4001889
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014
 15 F-NT2RP4001896
 F-NT2RP4001901//ESTs/1.4e-50:291:93//Hs.67991:AA147848
 F-NT2RP4001927
 F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:
 A379442
 20 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894
 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
 F-NT2RP4001953//ESTs/0.018:206:65//Hs.130105:AA904868
 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene
 25 for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:
 788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete
 cds//0.0019:279:65//Hs.159439:AF092047
 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.
 3826:U69560
 30 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139
 F-NT2RP4002052
 F-NT2RP4002058//ESTs/5.2e-41:347:72//Hs.121961:AA777873
 F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//
 Hs.100030:AF002999
 35 F-NT2RP4002075
 F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:
 AA325104
 F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654
 F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:W96684
 40 F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284
 F-NT2RP4002791//Alxatin 1//1.0:215:61//Hs.74520:X79204
 F-NT2RP4002888
 F-NT2RP4002905//ESTs/3.4e-50:280:94//Hs.131697:H14960
 F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995
 45 F-NT2RP5003461//ESTs/3.6e-10:45:98//Hs.88088:AA521071
 F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067
 F-NT2RP5003492
 F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//
 Hs.132884:AB006179
 50 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:
 AC004131
 F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542
 F-NT2RP5003522
 F-NT2RP5003524//ESTs/8.7e-08:340:62//Hs.152730:AI308943
 55 F-NT2RP5003534
 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:
 AB007934
 F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

- F-OVARC100006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]/[4.4e-75:355.99//Hs.36727:
AI051983
- F-OVARC100013//ESTs/[0.65:331.58//Hs.146326:AA534304
- F-OVARC100014//Homo sapiens CLE1 (CLE1) mRNA, complete cds/[1.8e-171:815.98//Hs.81449:AF058922
5 F-OVARC100017//Homo sapiens mRNA for NATAK, complete cds/[0.50:482.58//Hs.113264:AB005060
- F-OVARC100035//Homo sapiens CA17 protein mRNA, complete cds/[2.2e-37:238.89//Hs.69469:AF064603
- F-OVARC100058//ESTs/[1.1e-23:132.97//Hs.61809:AA503549
- F-OVARC100060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]/[6.7e-60:305.97//Hs.31696:
H50008
- 10 F-OVARC100068//ESTs/[3.8e-10:69.100//Hs.89048:AA282798
- F-OVARC100071//ESTs/[1.9e-36:202.95//Hs.125013:AA400543
- F-OVARC100085
- F-OVARC100087//EST/[1.0:199.58//Hs.122919:AA768442
- F-OVARC100091//Homo sapiens Jagged 2 mRNA, complete .cds/[0.00017:414.59//Hs.106387:AF029778
15 F-OVARC100092//ESTs/[4.6e-06:410.60//Hs.152250:AA203600
- F-OVARC100106//ESTs, Weakly similar to C25A1.1 [C.elegans]/[2.9e-73:406.92//Hs.109463:AI205174
- F-OVARC100109
- F-OVARC100113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds/[5.3e-
135:663.96//Hs.3688:AF062950
- 20 F-OVARC100114//Homo sapiens mRNA for KIAA0562 protein, complete cds/[3.4e-43:532.72//Hs.118401:
AB011134
- F-OVARC1000133//ESTs/[9.4e-50:249.98//Hs.159146:AI384010
- F-OVARC100139
- F-OVARC100145//ESTs/[1.6e-09:87.90//Hs.25219:AA291293
25 F-OVARC100148//ESTs/[4.4e-28:146.100//Hs.133223:AA677414
- F-OVARC100151
- F-OVARC100168//ESTs/[2.3e-48:264.95//Hs.14539:H67305
- F-OVARC100191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth
and development factor)/[0.10:50.59//Hs.154083:U70136
- 30 F-OVARC100198//ESTs/[1.3e-103:505.97//Hs.149341:AI249131
- F-OVARC100209//EST/[1.0:73.72//Hs.162600:AA594840
- F-OVARC100212//ESTs/[1.7e-17:121.91//Hs.50473:W68834
- F-OVARC100240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]
35 /[2.7e-31:264.79//Hs.151859:AA196379
- F-OVARC100241//Homo sapiens clone 23698 mRNA sequence/[3.4e-35:466.68//Hs.8136:U81984
- F-OVARC100288//TESTs, Weakly similar to Y53C12A.3 [C.elegans]/[0.00084:170.65//Hs.107747:AI357868
F-OVARC100302//EST/[4.1e-05:249.60//Hs.136432:AA555306
- F-OVARC100304//ESTs/[1.0:252.64//Hs.12126:AA203287
- F-OVARC100309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECUR-
40 SOR [Feltis catulus]/[0.51:193.66//Hs.6194:AI378579
- F-OVARC100321
- F-OVARC100326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds/[0.0018:507.60//
Hs.122359:AF051946
- F-OVARC1000335//ESTs/[9.3e-39:202.98//Hs.132849:AA779444
45 F-OVARC1000347
- F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1)
mRNA, 3' end of cds/[3.4e-06:353.62//Hs.121895:AF001450
- F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds/[0.94:231.64//Hs.156016:D50930
- F-OVARC1000411//EST/[0.43:234.59//Hs.124673:AA858162
50 F-OVARC1000414//EST/[5.2e-05:105.72//Hs.98827:AA435682
- F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds/[0.86:231.58//Hs.156016:D50930
- F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]/[1.7e-25:190.84//Hs.139513:AA259082
- F-OVARC1000431//ESTs/[0.041:356.57//Hs.139907:AA621615
- F-OVARC1000437//filamin 1 (actin-binding protein-280)/[0.93:281.60//Hs.76279:X53416
55 F-OVARC1000440//Human PINCH protein mRNA, complete cds/[8.8e-21:116.99//Hs.83987:U09284
- F-OVARC1000442//ESTs/[2.0e-19:207.78//Hs.134071:AI377423
- F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds/[3.2e-140:566.99//Hs.12334:
AB014583

F-OVARC1000461//ESTs//1.0e-39:215.95//Hs.131532:AI024524
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640
 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
 5 F-OVARC1000479
 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
 F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850
 F-OVARC1000526//ESTs//2.9e-08:368:611//Hs.42771:N26740
 10 F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475
 F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:
 15 66//Hs.85302:U76421
 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358
 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200
 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725
 20 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722
 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881
 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-
 plete cds//1.6e-78:424:93//Hs.86859:D43772
 25 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:
 AB011162
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639
 30 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.
 125315:AF027156
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306
 F-OVARC 1000700
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320
 35 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//
 1.2e-110:451:91//Hs.13476:AF038661
 F-OVARC1000730//ESTs. Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:
 AI141736
 F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411
 40 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196
 F-OVARC1000771//ESTs. Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//
 Hs.157059:W28130
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835
 45 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:
 AB014543
 50 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584
 F-OVARC1000862//ESTs. Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.
 159234:U89995
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143
 55 F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777
 F-OVARC 1000890
 F-OVARC1000891

F-OVARC1000897//ESTs//1.1e-07:145.69//Hs.119878:AA706818
 F-OVARC1000912//EST//3.6e-08:376.61//Hs.158782:AI376601
 F-OVARC1000915//*Homo sapiens* mRNA for KIAA0600 protein, partial cds//2.3e-85:419.97//Hs.9028:AF039691
 F-OVARC1000924//ESTs//3.6e-113:540.98//Hs.66058:AA424456
 5 F-OVARC1000936//*Human endogenous retrovirus envelope region mRNA (PL1)*//4.3e-64:623.72//Hs.114440:
 M11119
 F-OVARC1000937//EST//2.4e-39:170.96//Hs.129138:AA988078
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157.97//Hs.
 136243:AA307843
 10 F-OVARC 1000948
 F-OVARC1000959//EST//0.65:293.55//Hs.134725:AI088986
 F-OVARC1000960//*Ley I-LV1.4e-41:425.72*//Hs.37062:AC005952
 F-OVARC1000964//ESTs//1.4e-95:486.96//Hs.57079:D45288
 F-OVARC1000971//ESTs//0.19:198.62//Hs.153429:AI283069
 15 F-OVARC1000984//*Breakpoint cluster region protein BCR*//0.26:365.56//Hs.2557:Y00661
 F-OVARC1000996//*Human p300/CBP-associated factor (P/CAF) mRNA, complete* cds//6.8e-10:312.65//Hs.
 155302:U57317
 F-OVARC1000999//*Homo sapiens mRNA for chemokine LEC precursor, complete* cds//0.0056:209.62//Hs.10458:
 AF088219
 20 F-OVARC1001000//EST//4.2e-24:242.77//Hs.128952:AA984114
 F-OVARC1001004
 F-OVARC1001010
 F-OVARC1001011//ESTs, Moderately similar to *Tera* [M.musculus]//3.8e-47:234.99//Hs.110327:AA205866
 F-OVARC1001032//*HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2*//0.0076:
 25 624.57//Hs.75063:AL023584
 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578.89//Hs.111974:AI050735
 F-OVARC1001038//*Homo sapiens TRIAD1 type I mRNA, complete* cds//8.6e-152:733.97//Hs.9899:AF099149
 F-OVARC 1001040//ESTs//2.2e-38:204.96//Hs.128927:AI168074
 F-OVARC1001044//EST//0.036:304.61//Hs.137342:AA017385
 30 F-OVARC1001051
 F-OVARC1001055//*Human pre-B cell enhancing factor (PBEF) mRNA, complete* cds//1.1e-46:381.81//Hs.
 154968:U02020
 F-OVARC1001062//ESTs//0.020:265.60//Hs.146226:AI312873
 F-OVARC1001065//ESTs, Weakly similar to *C50F4.12* [C.elegans]//1.4e-21:183.84//Hs.46680:AA809451
 35 F-OVARC1001068//*Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial* cds//6.6e-132:620.98//Hs.
 3426:AF082657
 F-OVARC1001072//ESTs//1.1e-24:289.74//Hs.139614:AA709013
 F-OVARC1001074//ESTs//0.059:198.63//Hs.59974:AA001937
 F-OVARC1001085//*H.sapiens mRNA for sortilin*//0.99:142.67//Hs.104247:X98248
 40 F-OVARC1001092//*Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))*//1.3e-75:289.95//Hs.21753:AJ005897
 F-OVARC1001107//*Homo sapiens SKB1Hs mRNA, complete* cds//1.2e-73:351.86//Hs.12912:AF015913
 F-OVARC1001113//*Homo sapiens diaphanous 1 (HDIA1) mRNA, complete* cds//2.1e-151:710.98//Hs.26584:
 AF051782
 45 F-OVARC1001117//ESTs//3.8e-73:347.99//Hs.116029:AA813102
 F-OVARC1001118
 F-OVARC1001129
 F-OVARC1001154//*Granulin*//2.4e-94:686.83//Hs.75451:AF055008
 F-OVARC1001161//ESTs//2.2e-40:208.97//Hs.113006:AA621725
 50 F-OVARC1001162
 F-OVARC1001167
 F-OVARC1001169//ESTs//0.81:158.63//Hs.48527:AI078279
 F-OVARC1001170//ESTs//9.0e-87:412.99//Hs.116550:AA813287
 F-OVARC1001171//ESTs//4.9e-26:167.79//Hs.139158:AA226159
 55 F-OVARC1001173//ESTs, Moderately similar to *GLUTAMATE DEHYDROGENASE 1 PRECURSOR* [*Homo sapiens*]//1.8e-11:192.69//Hs.130020:AA887581
 F-OVARC1001176//*Homo sapiens chromosome 19, cosmid R26529*//0.61:387.58//Hs.91103:AC005551
 F-OVARC1001180//ESTs, Weakly similar to *ubiquitin S6(1)* [D.melanogaster]//1.5e-13:199.71//Hs.109966:

C06057
F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/|.1e-52:324:90//Hs.114673:W72675
F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889
5 F-OVARC1001232//Cyclin A/0.95:124:67//Hs.85137:X51688
F-OVARC1001240//EST/0.017:351:60//Hs.120655:AA745676
F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825
F-OVARC1001244//RING3 PROTEIN/2.8e-19:118:95//Hs.75243:D42040
F-OVARC1001261//EST/1.9e-42:225:95//Hs.158854:AI377837
10 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821
F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224
F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:
AB014543
F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]/|/0.11:355:60//Hs.108812:AA044835
15 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172
F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.
152455:AF044209
F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264
F-OVARC1001330
20 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like
1)|/0.021:232:62//Hs.79410:U62531
F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]/|/2.5e-76:363:99//Hs.105837:AA536054
F-OVARC1001342//EST/0.98:97:65//Hs.148210:AA897493
F-OVARC1001344//EST/5.3e-10:241:64//Hs.138777:N67251
25 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.109540:
AF004715
F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633
F-OVARC1001369//ESTs//3.3e-07:371:62//Hs.131653:AI025777
F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:
30 AB014554
F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.
129735:AF010144
F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//
Hs.151428:AJ224819
35 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:
65//Hs.25674:AF072242
F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225
F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651
F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426
40 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651
F-OVARC1001436
F-OVARC1001442
F-OVARC1001453
F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGEN-
45 IC REGION [S.cerevisiae]/|/1.9e-125:581:99//Hs.110950:AI041823
F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568
F-OVARC1001489//EST/4.9e-72:341:100//Hs.148191:AA897343
F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:
AF016507
50 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)/|/1.1e-97:538:92//Hs.75813:L33243
F-OVARC1001525
F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786
F-OVARC1001547//EST/0.0046:237:62//Hs.54638:N90595
F-OVARC1001555
55 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:
AF031166
F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/|/0.0035:
271:60//Hs.108465:AI144299

F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398
 F-OVARC1001611
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144
 5 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807
 10 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588
 F-OVARC1001762
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//
 15 1.4e-150:706:98//Hs.155377:U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:
 AB014575
 F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:AI218697
 F-OVARC1001791
 20 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:
 AB018287
 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.
 25 69949:M94172
 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453
 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567
 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537
 30 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973
 F-OVARC1001861
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:
 AF070611
 F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel sub-
 35 unit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709
 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127
 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.
 158095:AB007953
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//
 40 2.6e-57:300:96//Hs.6216:AF061749
 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834
 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261
 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263
 F-OVARC1001928
 45 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204
 F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III
 [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794
 F-OVARC1001949//KRAB zinc finger protein (alternative products)//1.8e-17:294:67//Hs.22556:U37251
 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228
 50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639
 F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:
 213:78/Hs.105292:AA504776
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:
 55 AB007934
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
 F-OVARC1002107

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498.96//Hs.75258:
AF054174
F-OVARC1002127//ESTs//1.6e-76:397.96//Hs.33432:R83913
F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399.62//Hs.112725:AF056022
5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868
F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:
X79568
10 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517
F-PLACE1000004//ESTs//0..79:332:59//Hs.120221:AA731230
F-PLACE1000005//ESTs//1..8e-10:89:87//Hs.158913:AI378928
F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.
42400:AF022789
15 F-PLACE1000014
F-PLACE1000031
F-PLACE1000040//ESTs//3..1e-18:123:91//Hs.138387:AA873088
F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
F-PLACE1000050//ESTs//1..8e-84:421:98//Hs.128632:AI076755
20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:
93//Hs.30026:AI356771
F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!! [H.sapiens]//6.4e-
15:203:70//Hs.157422:R85366
25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082
F-PLACE1000094
F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//
Hs.111081:AI380378
F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:
30 AA632135
F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.
151017:AF058291
F-PLACE1000185
F-PLACE1000213
35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255
F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
F-PLACE1000246//ESTs//7..3e-80:457:89//Hs.57209:W22022
F-PLACE1000292//ESTs//1..8e-05:323:60//Hs.59962:AI278202
F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
F-PLACE1000347//ESTs//6..4e-33:169:99//Hs.122975:AA428675
F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:
M37197
F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:
45 262:58//Hs.102732:U88153
F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516
F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPlicing FACTOR [Homo sapiens]//8.7e-63:346:
93//Hs.19501:AA742260
50 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:
U33053
F-PLACE1000424
F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590
55 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)
//2.7e-52:421:80//Hs.69747:M35531
F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638
F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353
 F-PLACE1000540//ESTs//0.32:229:59//Hs.163011:AA700573
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289
 5 F-PLACE1000562
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6..6e-47:525:72//Hs.21838:AF038179
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:
 10 AJ012449
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
 F-PLACE1000636
 15 F-PLACE1000653//Homo sapiens N-acetylgalactosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:
 96//Hs.5819:AF102265
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and
 LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:77:97//Hs.29595:AJ005896
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:
 20 69//Hs.128763:AF009353
 F-PLACE1000712//ESTs//0.56:171:61//Hs.112790:AA609949
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694
 25 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858
 F-PLACE1000769
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:
 AB014548
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215
 30 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000
 35 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201
 F-PLACE1000948
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.
 40 80261:L43821
 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88://
 Hs.13531:R61789
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)/0.0034:229:62//Hs.8597:L11672
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:
 45 AB018267
 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876
 50 F-PLACE1001024
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204
 F-PLACE1001062
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859
 55 F-PLACE1001088
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

71//Hs.150406.AF022158
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257.M30704
 F-PLACE1001168
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392.R95135
 5 F-PLACE1001185//ESTs. Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763.W30741
 F-PLACE1001238
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786.R49494
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518-AA913929
 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724.X70476
 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628.N51283
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:
 58//Hs.124161.AF065164
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.
 16533:D87930
 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672.AF016052
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384.Z78385
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120-AA699591
 F-PLACE1001351
 20 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638.AB018342
 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:
 AF009615
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501.AA973748
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:
 117:84//Hs.21301.AF093419
 25 F-PLACE1001387//ESTs. Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE
 EPS8 [H.sapiens]//0.00083:187:64//Hs.5399.N30646
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete
 CDS//0.0038:496:57//Hs.97681.AJ223333
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.
 30 154069.U06452
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:
 AF091087
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622.AA633232
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082.H18987
 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373.R09510
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536.AI379455
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992.H52716
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260.M12529
 F-PLACE1001503
 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352.AA718914
 F-PLACE1001534//EST//0.015:121:65//Hs.144156.R85753
 F-PLACE1001545
 F-PLACE1001551
 F-PLACE1001570//EST//0.58:286:59//Hs.120202.AA728835
 45 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266.U06233
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406.AF069987
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915.AI342230
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700.AA808005
 F-PLACE1001611//Human facioigenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572.U11690
 50 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:
 AB018341
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064.AI276198
 F-PLACE1001640
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341.AA810927
 55 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-
 148:726:96//Hs.3688.AF069250
 F-PLACE1001692//ESTs. Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN
 [Rattus norvegicus]//1.1e-95:481:92//Hs.24309.AI125696

F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.
101555:U93869

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776

F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686

5 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094

F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052

F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159

F-PLACE1001745

F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361

10 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:
AF061243

F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750

F-PLACE1001761//ESTs//6.2e-27:159:93//Hs.78277:AA131283

F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.
15 150981:U47050

F-PLACE1001781

F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115

F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
20 3.6e-110:546:96//Hs.40820:AF058953

F-PLACE1001821

F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494

F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214

F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906

25 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257

F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220

F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.
17839:AF099936

F-PLACE1001928//H.sapiens HUMMM9 mRNA//0.063:196:66//Hs.2750:X74837

30 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778

F-PLACE1001989

F-PLACE1002004

F-PLACE1002046

F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108

35 F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555

F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178

F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//
Hs.5171:AF069765

40 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637

F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831

F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:
75//Hs.144290:T61747

F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631

45 F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390

F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891

F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627

F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674

F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289

50 F-PLACE1002211//ESTs//0.041:146:67//Hs.119162:AA399989

F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442

F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935

F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503

F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675

55 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279

F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034281

F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710

F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458.66//Hs.40993:AF000148
 F-PLACE1002438//EST/0.81:48.77//Hs.158575:AI368947
 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:
 5 66//Hs.150406:AF022158
 F-PLACE1002465
 F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369.63//Hs.129361:AJ007581
 F-PLACE1002477//ESTs/3.5e-13:125.71//Hs.145032:AA343523
 F-PLACE1002493
 10 F-PLACE1002499
 F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708.59//Hs.
 11967:UT6010
 F-PLACE1002514//ESTs/3.1e-07:178.66//Hs.70932:AA126482
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583.95//Hs.88756:
 15 AB018256
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566.96//Hs.99348:
 AC004774
 F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198.86//Hs.51124:AF019369
 F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274.59//Hs.138202:AF027866
 20 F-PLACE1002578//ESTs/7.3e-10:185.73//Hs.41418:H90627
 F-PLACE1002583//EST/0.0028:348.61//Hs.160396:AI393725
 F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279.74//Hs.109606:
 D44497
 F-PLACE1002598//EST//0.011:209.62//Hs.131470:AI024187
 25 F-PLACE1002604//EST/0.47:220.61//Hs.145434:AI198915
 F-PLACE1002625
 F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693.62//Hs.80562:X04412
 F-PLACE1002665//EST//0.15:156.65//Hs.161793:AA380706
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:
 30 804.97//Hs.124903:AF068180
 F-PLACE1002714//Human involucrin mRNA//3.6e-08:509.60//Hs.157091:M13903
 F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230.58//Hs.159196:
 U92971
 F-PLACE1002768//EST//0.37:126.69//Hs.125353:AA877080
 35 F-PLACE1002772//ESTs/0.0017:147.69//Hs.132439:AA923728
 F-PLACE1002775//EST//5.5e-09:129.75//Hs.135336:AI049827
 F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298.62//Hs.26285:
 AF082516
 F-PLACE1002794//ESTs//0.71:125.66//Hs.97441:AI368926
 40 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567.70//Hs.77546:D79994
 F-PLACE1002815
 F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687.73//Hs.9028:AF039691
 F-PLACE1002834//ESTs//2.6e-41:393.74//Hs.120206:AI089163
 F-PLACE1002839//ESTs//0.26:177.63//Hs.149013:AI334167
 45 F-PLACE1002851//EST//0.0034:102.72//Hs.129630:AI000405
 F-PLACE1002853//ESTs//1.1e-20:136.90//Hs.125895:AA889024
 F-PLACE1002881//Interleukin 10/1.1e-41:454.72//Hs.2180:M57627
 F-PLACE1002908//ESTs/3.8e-48:325.88//Hs.54702:AI040029
 F-PLACE1002941//ESTs//5.0e-18:128.88//Hs.17376:AA855056
 50 F-PLACE1002962
 F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372.59//Hs.8021:AI041815
 F-PLACE1002991
 F-PLACE1002993
 F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104.86//Hs.124808:T86959
 55 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192.64//Hs.92660:
 AB007979
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632.97//Hs.129872:
 AB011088

F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555.58//Hs.154740:
AB014567
F-PLACE1003045
F-PLACE1003092//ESTs//1.1e-108:506.99//Hs.22119:AA885491
5 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650.73//Hs.102137:U31875
F-PLACE1003108//EST//0.016:181.65//Hs.119762:AA703419
F-PLACE1003136
F-PLACE1003145
F-PLACE1003153//ESTs//3.1e-09:209.65//Hs.111583:AA463590
10 F-PLACE1003174//ESTs//0.073:97.69//Hs.12992:W01997
F-PLACE1003176//ESTs//3.3e-60:296.90//Hs.58239:AA215797
F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:
221.60//Hs.139756:U59209
F-PLACE1003200//EST//0.0021:309.60//Hs.140561:AA765532
15 F-PLACE1003205//EST//1.2e-07:204.65//Hs.147372:AI208770
F-PLACE1003238//ESTs//7.4e-62:343.94//Hs.121302:AA758208
F-PLACE1003249//Insulin-like growth factor 1 (somatomedin C) //0.99:175.62//Hs.85112:X57055
F-PLACE1003256
F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217.64//Hs.29285:X99802
20 F-PLACE1003296//ESTs//2.6e-14:80.86//Hs.155441:AA533106
F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700.67//Hs.
37138:U35376
F-PLACE1003343
F-PLACE1003342//ESTs//0.94:310.57//Hs.131502:AI023308
25 F-PLACE1003343//EST//1.2e-09:114.77//Hs.103418:AA035568
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//
2.6e-144:77.92//Hs.6564:U92715
F-PLACE1003361//ESTs. Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:
78//Hs.163820:H71277
30 F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502.57//Hs.143897:AF075575
F-PLACE1003369//NUCLEOLIN//0.00037:282.60//Hs.79110:M60858
F-PLACE1003373//EST//1.1e-11:420.63//Hs.156592:AI343009
F-PLACE1003375//EST//0.75:119.68//Hs.160270:AI149069
F-PLACE1003383
35 F-PLACE1003394//ESTs. Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:
94//Hs.125175:AI142546
F-PLACE1003401//ESTs//0.55:176.66//Hs.154292:AA886178
F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206.62//Hs.30223:X90846
F-PLACE1003454//ESTs//0.98:74.72//Hs.127131:AA150912
40 F-PLACE1003478//EST//5.0e-06:183.69//Hs.127524:AA952874
F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232.63//Hs.90572:U33635
F-PLACE1003516//Human kpnl repeat mRNA (cdna clone pcd-kpnl-8), 3' end//3.4e-85:357.86//Hs.103948:K00627
F-PLACE1003519//ESTs//1.6e-33:288.72//Hs.159510:AA297145
F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269.76//Hs.6940:Z48633
45 F-PLACE1003528//ESTs//0.65:120.68//Hs.162376:AA570248
F-PLACE1003537//ESTs. Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543.97//Hs.120416:AA057428
F-PLACE1003553
F-PLACE1003566//ESTs//0.0015:508.59//Hs.5724:AA156780
F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499.58//Hs.65993:AF000367
50 F-PLACE1003583//ESTs//5.5e-19:448.63//Hs.161701:AA225932
F-PLACE1003584//EST//1.6e-46:263.94//Hs.147412:AI209194
F-PLACE1003592//ESTs. Moderately similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//1.4e-50:287:
93//Hs.154799:AA130620
F-PLACE1003593//ESTs//0.0025:318.61//Hs.106771:AA806965
55 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685.68//Hs.89650:L38961
F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679.97//Hs.56851:D83200
F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236.64//Hs.22116:
AF064104

F-PLACE1003611//EST/0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503
 F-PLACE1003625//ESTs/1.6e-16:103:96//Hs.11223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
 5 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:
 AF053305
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
 10 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:
 AJ000553
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:
 AI346344
 F-PLACE1003760//ESTs/5.1e-08:334:63//Hs.43675:AA805648
 15 F-PLACE1003762//ESTs/1.0:59:83//Hs.29863:W28983
 F-PLACE1003768//Human kpn1 repeat mRNA (cdna clone pcd-kpn1-4), 3' end//2.7e-40:608:68//Hs.139107:K00629
 F-PLACE1003771//ESTs//6.16e-10:226:65//Hs.15776:T91944
 F-PLACE1003783
 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308
 20 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169
 F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786
 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124
 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
 25 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770
 F-PLACE1003886
 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108
 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
 30 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
 F-PLACE1003915//ESTs, Highly similar to ARGINYLY-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR
 [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
 35 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:
 71//Hs.3136:U42412
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
 40 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi//0.85:164:64//Hs.
 153045:X52056
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:
 45 X04526
 F-PLACE1004149//ESTs, Weakly similar to FAF7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
 50 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//
 1.3e-145:695:98//Hs.24640:AF069493
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
 55 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.
 31718:N29128
 F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573.56//Hs.154139:
AB007914

F-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds//2.0e-157:756:
97//Hs.127007:AF084830

5 F-PLACE1004284//ESTs//3.6e-71:344.99//Hs.145870:AI2171884

F-PLACE1004289//ESTs//2.6e-57:370.85//Hs.16740:AA586576

F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513.59//Hs.83363:M34677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797.94//Hs.11171:Y11588

F-PLACE1004336

10 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:
688.97//Hs.16232:AF100153

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521.98//Hs.14079:AA306552

F-PLACE1004384//Human HsLIM15 mRNA for HsLIM15, complete cds//2.0e-49:466.76//Hs.37181:D64108

F-PLACE1004388

15 F-PLACE1004405//EST//0.010:191.64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.e-20:124.80//Hs.94195:W03579

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190

F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
encoding mitochondrial protein, complete cds//9.9e-131:536.99//Hs.155410:U49283

20 F-PLACE1004451//ESTs//5.9e-18:203.73//Hs.156097:AI348867

F-PLACE1004460

F-PLACE1004467//ESTs//8.0e-17:345.66//Hs.112993:AA824363

F-PLACE1004471//EST//9.3e-69:463.84//Hs.116391:AA644085

F-PLACE1004473//ESTs//0.93:358.58//Hs.33263:AA724416

25 F-PLACE1004491//EST//2.5e-58:285.99//Hs.97603:AA398163

F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228.63//Hs.54457:M33680

F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699.97//
Hs.122752:AF026445

F-PLACE1004516//EST//1.0e-26:343.71//Hs.142595:N24150

30 F-PLACE1004518

F-PLACE1004548//EST//0.84:193.62//Hs.99583:AA461314

F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627.94//Hs.107387:
AA058854

F-PLACE1004564//EST//1.0:240.62//Hs.168224:T91371

35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242.64//Hs.85004:X05299

F-PLACE1004645

F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386.63//Hs.2133:U18991

F-PLACE1004658//ESTs//0.52:273.61//Hs.97252:AA291590

F-PLACE1004664

40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//
1.5e-66:357.95//Hs.77705:U07563

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625.91//Hs.
80019:AF035606

F-PLACE1004681//EST//0.0092:303.61//Hs.149560:AI281589

45 F-PLACE1004686//ESTs//3.0e-31:186.76//Hs.139130:AA704561

F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242.61//Hs.48483:AF007131

F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96.71//Hs.125740:AA884845

F-PLACE1004716//ESTs//2.0e-79:388.98//Hs.150999:AI306542

F-PLACE1004722//ESTs//7.5e-06:105.72//Hs.128796:AA4485891

50 F-PLACE1004736//ESTs//1.7e-27:203.86//Hs.119593:AA700148

F-PLACE1004740//ESTs//1.0e-25:174.89//Hs.29696:AA910680

F-PLACE1004743

F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-
2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260.90//Hs.6863:W52470

55 F-PLACE1004773//Homo sapiens inverin protein mRNA, complete cds//1.7e-172:828.97//Hs.104715:AF084367

F-PLACE1004777//Human myosin Ixb mRNA, complete cds//1.0e-29:556.63//Hs.159629:U42391

F-PLACE1004793

F-PLACE1004804

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340
 F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284
 F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362
 5 F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047
 F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669
 F-PLACE1004838
 F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910
 10 F-PLACE1004868
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772
 F-PLACE1004900
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA504929
 15 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130
 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:
 AF099936
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592
 20 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
 F-PLACE1004969
 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:
 235:60//Hs.27610:U34605
 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:
 25 AB011147
 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520
 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831
 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459
 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159
 30 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943
 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:
 AB011148
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.
 35 122967:AF059569
 F-PLACE1005077//EST//0.79:283:591//Hs.89276:AA283899
 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740
 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:
 AB011147
 40 F-PLACE1005101//Homo sapiens (clone zapl28) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401
 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FB1) mRNA, complete cds//
 8.9e-18:538:62//Hs.104640:AF000561
 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366
 F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227
 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661
 F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:
 H11741
 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087
 F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:
 50 AB014541
 F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:
 AI138605
 F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417
 F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009
 55 F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//
 Hs.47334:W72370
 F-PLACE1005243
 F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds/5.1e-150:706:98//Hs.118087:
 AB011182
 F-PLACE1005287//ESTs/8.1e-107:501:99//Hs.145703:AA447947
 5 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL/4.4e-37:597:66//Hs.101642:
 X60673
 F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2/0.83:239:62//Hs.80684:X62534
 F-PLACE1005313
 F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]/6.0e-81:459:91//Hs.146177:
 10 R51650
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds/0.96:510:56//Hs.159183:AB018297
 F-PLACE1005373
 F-PLACE1005374//ESTs/7.5e-77:437:91//Hs.143266:AI141348
 15 F-PLACE1005409//ESTs/2.4e-05:267:63//Hs.163307:AA856751
 F-PLACE1005453//ESTs/0.12:333:58//Hs.134672:AI087951
 F-PLACE1005467//HOMEobox/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
 F-PLACE1005471//ESTs/3.4e-24:135:97//Hs.49275:N66925
 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503
 20 F-PLACE1005480//ESTs/3.7e-26:184:70//Hs.113198:N39323
 F-PLACE1005481//ESTs/0.27:153:64//Hs.120066:AA707973
 F-PLACE1005494//ESTs/2.40:50:257:98//Hs.159003:AA633029
 F-PLACE1005502//ESTs/0.15:408:57//Hs.45106:AA504105
 F-PLACE1005526//ESTs/3.2e-61:305:98//Hs.122574:AA776747
 25 F-PLACE1005528//ESTs/9.9e-32:249:78//Hs.142531:N91572
 F-PLACE1005530//ESTs/1.0e-94:491:95//Hs.131731:AI339335
 F-PLACE1005550//ESTs/0.084:290:58//Hs.157775:AI359385
 F-PLACE1005554//EST/0.38:213:58//Hs.102749:N64144
 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR
 30 [Saccharomyces cerevisiae]/4.5e-51:258:97//Hs.7736:W81261
 F-PLACE1005574//ESTs/3.2e-09:236:66//Hs.146884:AI160278
 F-PLACE1005584//Fragile X mental retardation 2/1.2e-05:151:69//Hs.54472:U48436
 F-PLACE1005595//ESTs/2.1e-98:512:95//Hs.118552:W74594
 F-PLACE1005603//EST/1.0:90:66//Hs.111204:AA211851
 35 F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]/3.5e-32:197:92//Hs.8241:AA283057
 F-PLACE1005623//ESTs/3.0e-30:191:92//Hs.77570:N48234
 F-PLACE1005630//ESTs/2.3e-32:175:97//Hs.122278:AA781867
 F-PLACE1005639//ESTs/0.88:218:58//Hs.117389:AA701991
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:
 40 AF083255
 F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
 F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds/0.086:223:59//Hs.27349:
 AB007917
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
 45 F-PLACE1005727//ESTs/8.7e-65:330:96//Hs.127027:AA935437
 F-PLACE1005730//ESTs/2.9e-14:270:67//Hs.28589:AI004944
 F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//
 Hs.75111:D87258
 F-PLACE1005755//Insulin-like growth factor binding protein 2/3.6e-05:377:62//Hs.162:X16302
 50 F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN
 [Rattus norvegicus]/7.5e-49:252:88//Hs.24309:AI125696
 F-PLACE1005799//ESTs/5.2e-13:392:58//Hs.110530:AA191493
 F-PLACE1005802
 F-PLACE1005803
 55 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:
 AF027156
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:
 AF065482

F-PLACE1005828//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]/4.1e-42:
 327.81/Hs.138404.R70986
 F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)/0.038:436:58//Hs.75770:L41870
 F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149.AI379497
 5 F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096_AA186905
 F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608_AA732242
 F-PLACE1005876//ESTs//0.97:282:60//Hs.98664.AI381487
 F-PLACE1005884//ESTs//0.070:276:60//Hs.106057.AI031552
 F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993.AA843300
 10 F-PLACE1005898
 F-PLACE1005921
 F-PLACE1005923//ESTs//0.50:308:58//Hs.52489.R61504
 F-PLACE1005925//ESTs//0.024:93:68//Hs.149868.AI288274
 F-PLACE1005932//TYROSINE-PROTEIN KINASE EPH PRECURSOR//0.97:342:57//Hs.89839:
 15 M18391
 F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092-AA922142
 F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978
 F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522.M92357
 F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996.R73468
 20 F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]/0.15:136:66//Hs.107747.AI357868
 F-PLACE1005966//Human zinc fmger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:
 U13948
 F-PLACE1005968
 F-PLACE1005990
 25 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674.U61981
 F-PLACE1006003//EST//0.00018:171:67//Hs.138882.W73256
 F-PLACE1006011
 F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173.AA757743
 F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:
 30 AB018332
 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782.X99906
 F-PLACE1006076//EST//0.29:92:64//Hs.161536.N80395
 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:
 AF039023
 35 F-PLACE1006129
 F-PLACE1006139
 F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014.AB002353
 F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]/2.9e-12:119:84//Hs.23153:
 R92857
 40 F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740.H17868
 F-PLACE10061641//ESTs//0.099:223:60//Hs.8108_AA902721
 F-PLACE10061671//Homo sapiens chromosome 19, cosmid C23149//1.1e-68:333:92//Hs.152894.AC005239
 F-PLACE1006170//ESTs//0.081:171:67//Hs.135187.AI074005
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464.AF091433
 45 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470.N49608
 F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.
 135623.AA134719
 F-PLACE1006205
 F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]
 50 //0.0089:166:63//Hs.127179.AI279486
 F-PLACE1006225
 F-PLACE1006236//EST//0.060:89:69//Hs.136977.AA830668
 F-PLACE1006239//ESTs//0.028:105:66//Hs.142336_AA358185
 F-PLACE1006246//ESTs//0.060:330:60//Hs.105695.AI085802
 55 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:
 AB014548
 F-PLACE1006262
 F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277.AJ001625

F-PLACE1006318
F-PLACE1006325//ESTs/3.7e-25:206.83//Hs.102319:AI246503
F-PLACE1006335//ESTs/2.0e-27:161.95//Hs.163529:AI361492
F-PLACE1006357//ESTs/0.013:268.61//Hs.105775:AA526249
5 F-PLACE1006360//ESTs/4.8e-27:146.98//Hs.100739:Z98481
F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272.59//Hs.153529:AF070581
F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403.61//Hs.105940:
AF004715
F-PLACE1006382//EST/0.98:77.68//Hs.136933:AA814693
10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539.97//Hs.22396:AF062085
F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424.74//Hs.21560:AB002296
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525.98//Hs.
131846:AF069735
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531.65//Hs.101414:
15 AB011129
F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//
1.0:248.60//Hs.88219:AF060866
F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381
F-PLACE1006470
20 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//
5.0e-46:520.71//Hs.131953:AF059194
F-PLACE1006488//ESTs/6.2e-47:239.97//Hs.158161:AA312511
F-PLACE1006492//ESTs/0.82:37:100//Hs.160417:AA488493
F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:
25 56//Hs.75063:AL023584
F-PLACE1006521//ESTs/0.032:222.63//Hs.23171:AA706542
F-PLACE1006531//EST//2.1e-53:258.100//Hs.117316:AA699358
F-PLACE1006534//EST//1.8e-07:78.89//Hs.157551:AI356219
F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383.58//Hs.32963:D31784
30 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464.57//Hs.1540:L36529
F-PLACE1006598//Homo sapiens mRNA for KIAA0731 protein, complete cds//4.1e-17:372.65//Hs.17630:
AB018280
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//
2.2e-168:781.99//Hs.155377:U98760
35 F-PLACE1006617//ESTs/6.0e-08:354.60//Hs.42624:H99088
F-PLACE1006626//NUCLEOLIN//0.0044:186.66//Hs.79110:M60858
F-PLACE1006629//Homo sapiens (clone s2271) mRNA fragment//0.097:229.63//Hs.26956:L40396
F-PLACE1006640//ESTs/0.00019:380.59//Hs.13672:AI131473
F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113.83//Hs.3385:N25917
40 F-PLACE1006678
F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284.60//Hs.153638:AF010403
F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382.63//Hs.43627:
U35612
F-PLACE1006754//Biliary glycoprotein//8.9e-27:305.72//Hs.50964:X16354
45 F-PLACE1006760//ESTs/0.10:207.62//Hs.152589:AA954152
F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251.64//Hs.89591:M97252
F-PLACE1006782//ESTs/1.2e-90:423.100//Hs.132826:AI075783
F-PLACE1006792//ESTs/1.5e-10:439.58//Hs.138501:AI051228
F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84.95//Hs.
50 123642:M83941
F-PLACE1006800//ESTs/0.00068:360.61//Hs.157876:AI422017
F-PLACE1006805//ESTs/4.6e-103:491.98//Hs.140465:AA769892
F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403.56//Hs.15832:AB014518
F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619.87//Hs.23094:M19503
55 F-PLACE1006829//ESTs/1.5e-22:144.94//Hs.142988:AA142876
F-PLACE1006860//EST//0.0062:206.65//Hs.158793:AI376773
F-PLACE1006867//ESTs/0.068:218.62//Hs.91166:AA551273
F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268.58//Hs.5333:AB018254

F-PLACE1006863//ESTs/1.6e-75:398.94//Hs.119544:T95801
 F-PLACE1006901//ESTs/1.9e-13:87.96//Hs.134737:AI089187
 F-PLACE1006904//EST/1.0:91:70//Hs.148270:AA906443
 F-PLACE1006917
 5 F-PLACE1006932//ESTs/0.98:110:70//Hs.100855:AI423913
 F-PLACE1006935//EST/1.0:92:65//Hs.124554:AA847211
 F-PLACE1006956//PERIPHERIN/0.13:443:57//Hs.37044: L14565
 F-PLACE1006958//Heat shock 70kD protein 4/6.4e-40:456:70//Hs.127:L12723
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]/3.2e-07:67.98//Hs.
 10 21806:AA630312
 F-PLACE1006962//H.sapiens ir1B mRNA/2.3e-16:202:71//Hs.135202:X63417
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds/0.14:
 191:67//Hs.8813:AF032922
 F-PLACE1006969//Cyclin B1//0.99:224:59//Hs.23960:M25753
 15 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//
 3.1e-05:594.58//Hs.32951:AF034102
 F-PLACE1007021//ESTs/7.2e-89:446.96//Hs.7111:U55971
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503
 F-PLACE1007053//Homo sapiens mRNA for ARN03 protein//0.35:63.82//Hs.129811:AJ223957
 20 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.57813:L33243
 F-PLACE1007097//ESTs/2.9e-25:197.83//Hs.105665:H78987
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-
 gen storage disease type III)/0.18:268:63//Hs.904:U84010
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385
 25 F-PLACE1007112
 F-PLACE1007132//ESTs/3.1e-30:195.76//Hs.46158:AI160121
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601
 F-PLACE1007178//ESTs/9.6e-54:289.95//Hs.12251:H12965
 30 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669
 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204
 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//
 Hs.80598:D50495
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
 F-PLACE1007243//ESTs/2.0e-43:227:97//Hs.124775:AA648467
 35 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909
 F-PLACE1007274
 F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167.64//Hs.606:
 L06133
 F-PLACE1007282
 40 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//
 Hs.144877:AF029403
 F-PLACE1007342
 45 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:
 567:98//Hs.76596:AF096870
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642
 50 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//
 Hs.14387:AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436
 55 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

F-PLACE1007484//ESTs/1.1e-18:127:91//Hs.100251:AA535975
F-PLACE1007488
F-PLACE1007507//ESTs/1.2e-99:274:98//Hs.123462:AA903385
F-PLACE1007511//Keratin/19/4.2e-31:586:64//Hs.23761:Y00503
5 F-PLACE1007524//ESTs/6.8e-71:356:97//Hs.163067:AA897296
F-PLACE1007525//ESTs/0.073:242:59//Hs.128711:AA856979
F-PLACE1007537//*Homo sapiens* PYRIN (MEV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080
F-PLACE1007544//ESTs/1.1e-74:360:98//Hs.128632:AI076755
F-PLACE1007547//*Homo sapiens* mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:
10 AB014561
F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863
F-PLACE1007583//ESTs/1.8e-46:234:98//Hs.155071:AA584257
F-PLACE1007598//ESTs/1.7e-83:400:99//Hs.120206:AI089163
F-PLACE1007618//*Homo sapiens* mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533
15 F-PLACE1007621
F-PLACE1007632//ESTs/1.7e-32:175:97//Hs.122278:AA781867
F-PLACE1007645
F-PLACE1007649
F-PLACE1007677//ESTs/3.0e-13:125:82//Hs.143382:AA476266
20 F-PLACE1007688//ESTs/6.8e-06:311:61//Hs.132926:AI027055
F-PLACE1007690//ESTs/1.9e-13:83:98//Hs.150088:AI348503
F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812
F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953
F-PLACE1007706//*Homo sapiens* metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:
25 AF061243
F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:
AA476815
F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:
64//Hs.104128:AA923278
30 F-PLACE1007730//*Homo sapiens* mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:
AB014585
F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424
F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030
F-PLACE1007746//ESTs/6.7e-55:330:89//Hs.153392:AI089469
35 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656
F-PLACE1007807//ESTs/2.0e-54:385:83//Hs.163930:AA640504
F-PLACE1007810//ESTs/6.1e-53:416:81//Hs.152395:AA533107
F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841
F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635
40 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503
F-PLACE1007852
F-PLACE1007858//*Homo sapiens* mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:
AB018309
F-PLACE1007866//ESTs/3.0e-50:333:86//Hs.15792:AI038387
45 F-PLACE1007877
F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943
F-PLACE1007908//*Homo sapiens* mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.
92381:AB007956
F-PLACE1007946//ESTs/8.9e-16:250:68//Hs.88527:N24002
50 F-PLACE1007954//ESTs/1.6e-05:76:90//Hs.63314:AA056538
F-PLACE1007955//*Homo sapiens* cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.
5671:AF084530
F-PLACE1007958//*Homo sapiens* cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:
730:98//Hs.78106:AF079529
55 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:
W28567
F-PLACE1007990//ESTs/1.2e-104:493:99//Hs.118445:AI097043
F-PLACE1008000//*Homo sapiens* veli 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

F-PLACE1008002//ESTs/0.52:236:59//Hs.134292-AA603031
 F-PLACE1008044
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075-X60382
 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:
 5 U44060
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:
 U60975
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.
 10 100431:AF044197
 F-PLACE1008122//ESTs/0.95:198:60//Hs.126776:N28769
 F-PLACE1008129//ESTs/1.1e-99:499:96//Hs.131807-AA278874
 F-PLACE1008132//EST/3.3e-27:218:83//Hs.145258:AI218683
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.e-
 20:124:95//Hs.146238:AI263135
 15 F-PLACE1008181//ESTs/0.018:285:61//Hs.88843:AA281427
 F-PLACE1008198//ESTs/5.9e-07:410:60//Hs.63348:AA643524
 F-PLACE1008201
 F-PLACE1008209
 F-PLACE1008231//ESTs/0.40:188:61//Hs.130266:AI001856
 20 F-PLACE1008244//Miller-Dieker syndrome chromosome region/0.22:247:61//Hs.77318:L13385
 F-PLACE1008273
 F-PLACE1008275//EST/0.77:74:71//Hs.145907:AI275113
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.
 158987:AB007970
 25 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//10.16:263:63//Hs.
 4076:AF081287
 F-PLACE1008329//EST/1.3e-09:94:85//Hs.144135:R82071
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:
 AB011129
 30 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:
 AF059569
 F-PLACE1008369//ESTs/0.00074:443:61//Hs.102756:AA526911
 35 F-PLACE1008392//EST/7.4e-08:324:60//Hs.149930:AI289171
 F-PLACE1008398
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:
 62//Hs.25674:AF072242
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326
 40 F-PLACE1008405//ESTs/2.8e-102:529:95//Hs.116278:AA628943
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene cod-
 ing for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacyl/proline Aminopeptidase) and a novel
 gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653
 F-PLACE1008426//ESTs/3.2e-77:393:95//Hs.37585:W28499
 45 F-PLACE1008429//orf15' to PD-ECGF/TP..orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431,
 mRNA, 3 genes, 1718 nt]/0.019:530:58//Hs.72248:S72487
 F-PLACE1008437
 F-PLACE1008455//ESTs/0.51:279:61//Hs.122319:AA782335
 F-PLACE1008457//ESTs/3.0e-30:229:75//Hs.60740:AA053901
 50 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381
 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:
 U10886
 F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.0:304:
 60//Hs.24040:AF006823
 55 F-PLACE1008531//ESTs/1.1e-17:190:76//Hs.156041:AI274697
 F-PLACE1008532//Thromboxane A2 receptor/5.6e-17:231:71//Hs.89887:D38081
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter/1.1e-45:507:71//Hs.8003:AC004997
 F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

F-PLACE1008584//ESTs/1.4e-13:252.68//Hs.153429:AI283069
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175.812:98//Hs.23255:
 AB018334
 F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350.66//Hs.151087:
 5 AA649326
 F-PLACE1008625//ESTs/0.86:269:57//Hs.94998:N26794
 F-PLACE1008626//ESTs/0.55:69.71//Hs.92096:F10560
 F-PLACE1008627//ESTs/3.0e-62:302:99//Hs.120766:H82458
 F-PLACE1008629//ESTs/0.0012:174:67//Hs.121195:AA757211
 10 F-PLACE1008630//ESTs/4.5e-77:371:99//Hs.132960:AA252394
 F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.
 147967:AF044333
 F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728
 15 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit pre-
 cursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:
 AF038406
 F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741
 F-PLACE1008748//ESTs/0.88:204:63//Hs.15139:AA527080
 20 F-PLACE1008757//ESTs, Weakly similar to unknown protein R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:
 AF060543
 F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772
 F-PLACE1008807//ESTs/0.81:346:58//Hs.116901:AA663542
 25 F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:
 376:98//Hs.7179:AF011905
 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883
 F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium fal-
 ciparum (isolate K1 / thailand)]//0.73:354:59//Hs.26322:AA156858
 30 F-PLACE1008854//ESTs/3.0e-26:391:66//Hs.133260:AI052728
 F-PLACE1008867//ESTs/5.9e-08:64:93//Hs.91115:AI221563
 F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503
 F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA2862323
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:
 35 AB018308
 F-PLACE1008925//ESTs/0.025:133:67//Hs.103218:W84771
 F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026
 F-PLACE1008941//ESTs/3.3e-53:266:98//Hs.108677:AA488937
 F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:
 40 U75308
 F-PLACE1009020//ESTs/3.3e-11:122:81//Hs.131777:AI024950
 F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112
 F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762
 F-PLACE1009045//ESTs/2.2e-26:399:95//Hs.114919:AA457689
 45 F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:
 S70585
 F-PLACE1009050//ESTs/1.4e-92:451:98//Hs.66373:AI239698
 F-PLACE1009060//ESTs/1.4e-14:86:100//Hs.131725:AI090525
 F-PLACE1009090//ESTs/2.7e-20:198:78//Hs.110044:AA181800
 50 F-PLACE1009091//ESTs/0.99:342:57//Hs.46903:AI093091
 F-PLACE1009094//ESTs/1.0:225:63//Hs.120374:AI337031
 F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011
 F-PLACE1009110//ESTs/2.6e-91:453:96//Hs.143756:AI040890
 F-PLACE1009111//ESTs/2.7e-15:159:77//Hs.146811:AA410788
 55 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//
 1.1e-139:671:97//Hs.99742:AF035586
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215
 F-PLACE1009150//Human HsLIM15 mRNA for HsLIM15, complete cds//1.7e-50:440:78//Hs.37181:D64108

F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484/4.0e-46:440.69//Hs.158095:AB007953
 F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245.61//Hs.92614:M62302
 5 F-PLACE1009166//EST//0.98:114.67//Hs.137706:AA977250
 F-PLACE1009172//EST//6.2e-34:257.84//Hs.161081:N22770
 F-PLACE1009174//ESTs//6.0e-24:234.77//Hs.155196:AI282821
 F-PLACE1009183//EST//0.021:261.62//Hs.144222:N90100
 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588.95//Hs.54943:
 10 Z78396
 F-PLACE1009190//EST//0.046:95.70//Hs.131646:AI025689
 F-PLACE1009200//EST//2.5e-41:195.78//Hs.162404:AA573131
 F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSORS//5.3e-29:157.77//Hs.146403:M29540
 F-PLACE1009246//EST//0.13:178.62//Hs.23298:R22575
 15 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121.98//Hs.124768:AA307735
 F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195.62//Hs.148101:M88338
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:
 59//Hs.23731:U83192
 20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594.86//Hs.23094:M19503
 F-PLACE1009335//EST//0.037:169.63//Hs.148875:AI240767
 F-PLACE1009338//ESTs//5.7e-22:123.98//Hs.66783:AA059473
 F-PLACE1009368
 F-PLACE1009375
 25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317.81//Hs.43681:AL022394
 F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730.74//Hs.9450:M27878
 F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207.61//Hs.101174:AF047863
 F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210.86//Hs.3404:AF035262
 F-PLACE1009434//HUMAN mRNA for KIAA0005 gene, complete cds//2.8e-45:599.68//Hs.155291:D13630
 30 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350.58//Hs.82128:AJ012159
 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146.93//Hs.76987:AF012872
 F-PLACE1009459//H.sapiens garp gene mRNA, complete CDS//1.0:241.60//Hs.151641:Z24680
 F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//
 0.00039:347.60//Hs.994:M95678
 35 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67Al//4.1e-91:464.96//Hs.155049:
 AC004531
 F-PLACE1009477//ESTs//0.30:221.61//Hs.107287:AI308839
 F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608.63//Hs.16165:AB002405
 F-PLACE1009524//Human Sec7-like protein mRNA, partial cds//2.3e-68:526.78//Hs.8517:U70728
 40 F-PLACE1009539//ESTs//3.3e-18:186.83//Hs.71922:AA148417
 F-PLACE1009542//EST//7.8e-11:265.65//Hs.159692:AI416956
 F-PLACE1009571//ESTs//6.1e-15:94.97//Hs.151458:AA600866
 F-PLACE1009581//Microtubule-associated protein 1A//1.0:196.59//Hs.147918:U38291
 F-PLACE1009595//EST//1.8e-28:179.92//Hs.60090:AA004806
 45 F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281.66//Hs.13889:AI341394
 F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313.79//Hs.113283:AF018080
 F-PLACE1009613//ESTs//0.50:297.60//Hs.25114:AI074011
 F-PLACE1009621//ESTs//1.4e-98:470.98//Hs.124695:AI094085
 F-PLACE1009622//ESTs//9.8e-14:94.93//Hs.117227:AA682773
 50 F-PLACE1009637//ESTs//4.9e-92:440.98//Hs.126587:AA917087
 F-PLACE1009639
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816.98//Hs.21862:
 AB011159
 F-PLACE1009665//ESTs//9.1e-45:383.79//Hs.61199:AA024494
 55 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701.98//Hs.109590:AF062534
 F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN
 HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295.92//Hs.48541:AA827926
 F-PLACE1009721//EST//0.18:467.58//Hs.124358:AA830650

F-PLACE1009731//ESTs/1.0.207:63//Hs.60440:AA195789
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds/1.3e-126.602:98//Hs.154320:AF046024
 F-PLACE1009794//ESTs/4.0e-41:252:91//Hs.42927:N20989
 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-
 5 quone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs/5.5e-
 130:600:95//Hs.16411:AL030996
 F-PLACE1009845
 10 F-PLACE1009861
 F-PLACE1009879//ESTs/6.3e-12:293:66//Hs.147071:AI200021
 F-PLACE1009886
 F-PLACE1009888//EST/0.044:255:58//Hs.160695:AI282889
 F-PLACE1009908
 15 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717
 F-PLACE1009924//EST/2.9e-29:155:99//Hs.162937:AA634379
 F-PLACE1009925
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153
 F-PLACE1009947//ESTs/1.8e-07:56:100//Hs.149940:AI306446
 20 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345
 F-PLACE1009992//ESTs/0.99:123:68//Hs.91202:AI139114
 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds/3.7e-36:196:96//Hs.153545:
 AB014529
 25 F-PLACE1010023
 F-PLACE1010031//ESTs/1.3e-16:132:87//Hs.46847:W02878
 F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.
 142151:AA984061
 F-PLACE1010069//ESTs/6.6e-33:171:98//Hs.128844:AA977596
 30 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:
 AF065482
 F-PLACE1010076//ESTs/0.88:379:55//Hs.5884:Z21424
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds/9.6e-154:727:98//Hs.5003:AB007925
 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus
 35 musculus]//1.8e-38:212:95//Hs.98067:AA236822
 F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:
 U69567
 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds/0.0035:339:60//Hs.129683:
 AF020761
 40 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.
 122967:AF059569
 F-PLACE1010106//EST/8.5e-28:394:70//Hs.142044:AA166682
 F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889
 F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740
 45 F-PLACE1010152
 F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792
 F-PLACE1010194//ESTs/2.6e-55:284:97//Hs.159940:AA459582
 F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:
 H69637
 50 F-PLACE1010231
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:
 AB007917
 F-PLACE1010270//ESTs/2.0e-104:514:98//Hs.124062:H04590
 F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540
 55 F-PLACE1010293//EST/4.5e-36:358:74//Hs.162398:AA572813
 F-PLACE1010310//HOMEOPROPOU DOMAIN PROTEIN RDC 1//2.1e-10:352:62//Hs.74095:L20433
 F-PLACE1010321//Human hSIAH2 mRNA, complete cds/0.071:604:58//Hs.20191:U76248
 F-PLACE1010324//ESTs/0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST/|5.7e-05:351:60||Hs.120644:AA742659
 F-PLACE1010341//EST/|4.5e-16:255:72||Hs.141206:H53117
 F-PLACE1010362//ESTs/|1.9e-41:246:92||Hs.128771:AA236855
 F-PLACE1010364//EST/|0.11:292:58||Hs.135771:AI005648
 5 F-PLACE1010383//EST/|8.1e-08:107:76||Hs.136441:AA564986
 F-PLACE1010401
 F-PLACE1010481//Human BLU protein (BLU) mRNA, complete cds/|0.94:254:61||Hs.125257:U70824
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds/|7.2e-152:702:99||Hs.13313:
 AF039081
 10 F-PLACE1010492//ESTs/|1.0:201:60||Hs.146036:AI038500
 F-PLACE1010522//ESTs/|3.9e-52:263:97||Hs.125149:AI302100
 F-PLACE1010529//EST/|0.11:292:58||Hs.135771:AI005648
 F-PLACE101054177
 15 F-PLACE1010547//ESTs/|0.96:288:57||Hs.87156:AA233472
 F-PLACE1010562//EST/|1.0:164:66||Hs.147868:AI222979
 F-PLACE1010579//EST/|0.39:279:58||Hs.158960:AI380148
 F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06
 [Schizosaccharomyces pombe]/|3.8e-31:193:91||Hs.145229:AA44661
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete
 20 cds/|9.9e-148:707:97||Hs.19851:AF045186
 F-PLACE1010616//EST/|3.1e-43:213:100||Hs.128215:AA972394
 F-PLACE1010622//NUCLEOLIN/|0.00040:282:60||Hs.79110:M60858
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds/|1.2e-05:516:61||Hs.106387:AF029778
 F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]/|0.012:258:62||Hs.144375:AA484200
 25 F-PLACE1010629//EST/|8.3e-23:218:79||Hs.161975:AA501461
 F-PLACE1010630//EST/|0.29:319:58||Hs.137277:N62225
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds/|9.5e-66:363:95||Hs.10801:AB011102
 F-PLACE1010661//ESTs/|3.9e-89:504:92||Hs.122666:W27076
 F-PLACE1010662
 30 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds/|1.1e-74:697:74||Hs.
 37138:U35376
 F-PLACE1010714//EST/|0.018:253:59||Hs.148028:AI270027
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds/|6.1e-77:393:
 96||Hs.50758:AF092564
 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial/|0.97:314:59||Hs.14574:
 AJ131244
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds/|2.4e-56:409:86||Hs.159629:U42391
 F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus lae-
 vis]/|5.1e-80:407:96||Hs.80965:AA493284
 40 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]
 /|6.0e-45:251:94||Hs.11379:AA594140
 F-PLACE1010786
 F-PLACE1010800
 F-PLACE1010802//EST/|0.94:128:64||Hs.120366:AA719157
 45 F-PLACE1010811//ESTs/|0.89:339:59||Hs.127314:N48085
 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]/|2.9e-28:245:79||Hs.
 132736:AA583494
 F-PLACE1010856//ESTs/|1.5e-06:95:87||Hs.17401:W81048
 F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]/|5.8e-67:336:97||Hs.
 50 130135:AA905493
 F-PLACE1010870//Zinc finger protein 43 (HTF6)/|9.7e-40:498:69||Hs.74107:X59244
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds/|3.7e-149:694:98||Hs.118087:
 AB011182
 F-PLACE1010891//ESTs/|6.9e-54:377:87||Hs.24453:R31671
 55 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds/|0.64:167:65||Hs.1050:M85169
 F-PLACE1010900
 F-PLACE1010916//EST/|0.55:151:66||Hs.145800:AI269981
 F-PLACE1010917

F-PLACE1010925//ESTs/2.6e-81:437.94//Hs.5876:H26537
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653.98//Hs.74750:
 AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437.98//Hs.66392:
 5 AF064244
 F-PLACE1010944//ESTs/1.3e-17:117.91//Hs.29444:W30985
 F-PLACE1010947//EST//0.97:93.72//Hs.162299:AA555154
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444.59//Hs.585:X04506
 F-PLACE1010960//ESTs/0.98:238.60//Hs.163674:AA506632
 10 F-PLACE1010965//ESTs/3.1e-74:376.96//Hs.115679:AI379721
 F-PLACE1011026//EST//0.022:222.60//Hs.47154:N50931
 F-PLACE1011032//EST//1.1e-05:88.79//Hs.118024:N34032
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179.67//Hs.1177:
 U10886
 15 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-
 11:207.68//Hs.994:M95678
 F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310.78//Hs.2407:Z49194
 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228.61//
 Hs.153640:U56998
 20 F-PLACE1011057//EST//2.5e-80:388.98//Hs.126466:AA913320
 F-PLACE1011090//ESTs/1.4e-94:469.97//Hs.106448:R76663
 F-PLACE1011109//ESTs/0.13:303.62//Hs.49294:AA418037
 F-PLACE1011114//ESTs//5.8e-12:75.100//Hs.147422:AI214317
 F-PLACE1011133//ESTs//0.17:225.62//Hs.132853:AI370857
 25 F-PLACE1011143//ESTs/0.013:264.63//Hs.115368:AA629949
 F-PLACE1011160
 F-PLACE1011165//Galactokinase 2//2.7e-32:194.92//Hs.129228:M84443
 F-PLACE1011185//EST//1.4e-34:261.83//Hs.140250:AA708114
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-
 30 124:576.99//Hs.159140:AF038664
 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469.99//Hs.8241:AA283057
 F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221:
 88//Hs.101821:W27452
 F-PLACE1011221//ESTs//0.46:238.62//Hs.32853:AA015751
 35 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675.99//Hs.23168:
 AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from p721//5.9e-71:350.98//Hs.15144:AC005014
 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803
 F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191.65//Hs.140950:
 40 AF070637
 F-PLACE1011296//ESTs//0.019:137.63//Hs.140654:AA865915
 F-PLACE1011310//EST//0.068:336.58//Hs.162529:AA584160
 F-PLACE1011325//ESTs//7.4e-43:229.96//Hs.21081:H08310
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:
 45 99//Hs.5819:AF102265
 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.
 158897:AB007970
 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684.63//Hs.76415:D38535
 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325.99//
 50 Hs.107245:AA627053
 F-PLACE1011389//ESTs//8.6e-05:285.61//Hs.130105:AA904868
 F-PLACE1011419//ESTs//0.70:240.62//Hs.159650:N95552
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743.98//Hs.10801:
 AB011102
 55 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557.72//Hs.23094:M19503
 F-PLACE1011465//EST//3.1e-58:380.85//Hs.131605:AI025204
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703.99//Hs.111138:
 AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:
AF065482

F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264

F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997

5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319

F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476

F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:
268:86//Hs.86371:AF054180

10 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:
65//Hs.143641:AB009462

F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778

F-PLACE1011641

F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631

15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661

F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086

F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

20 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350

F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

25 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

30 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913

F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868

F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA958517

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:
35 AF059617

F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763

F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514

F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591

F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514

40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:
AB018256

F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.
92381:AB007956

F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503

45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330

F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627

F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831

F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627

F-PLACE2000017

50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//
5.7e-85:844:72//Hs.7928:AF082557

F-PLACE2000030

F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512

F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179

55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204

F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128

F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966

F-PLACE2000061

F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:MS8457
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:
 AF027219
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333
 5 F-PLACE2000100
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219
 F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:
 U56417
 F-PLACE2000115
 10 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353
 F-PLACE2000132
 F-PLACE2000136//ESTS, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:
 AA718911
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645
 15 F-PLACE2000164
 F-PLACE2000170
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179
 F-PLACE2000176
 F-PLACE2000187
 20 F-PLACE2000216
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:
 25 AB007958
 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
 F-PLACE2000317
 30 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for beta polypeptide//6.1e-24:295:76//Hs.30:
 M89796
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088
 F-PLACE2000342//Centromere protein B (80kD)/1.4e-06:326:61//Hs.85004:X05299
 F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817
 35 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI538861
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638
 40 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.
 158095:AB007953
 F-PLACE2000398
 F-PLACE2000399
 F-PLACE2000404
 45 F-PLACE2000411
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
 F-PLACE2000427
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
 50 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-
 20:418:64//Hs.130181:X85019
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080
 F-PLACE2000455//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//4.0e-
 55 05:100:73//Hs.104239:AA488082
 F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

F-PLACE3000004//Human EVA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262,
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)/0.00081:500:61//Hs.393:D38128
 F-PLACE3000029
 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
 F-PLACE3000070//ESTs/5.6e-15:202:74//Hs.154993:AA142842
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.
 122752:AF026445
 F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
 10 F-PLACE3000121
 F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
 F-PLACE3000145//ESTs/3.5e-25:145:96//Hs.163950:AI683016
 15 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
 F-PLACE3000148
 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:
 AB014572
 F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336203
 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:
 U79666
 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:
 AB011147
 F-PLACE3000160
 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
 F-PLACE3000194
 F-PLACE3000197
 F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//
 Hs.77522:X62744
 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
 F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-
 35 56:200:85//Hs.133089:AF064019
 F-PLACE3000226
 F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-
 40 Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene
 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase)LIKE pseudogene. Contains ESTs, STSs and ge-
 nomic marker DXS8032/1.2e-54:434:80//Hs.4943:Z98046
 F-PLACE3000244
 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
 F-PLACE3000271//ESTs/1.6e-25:195:72//Hs.108452:H76650
 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944
 F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770
 F-PLACE3000310
 F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586
 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
 50 F-PLACE3000331
 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:
 AB014545
 F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741
 F-PLACE3000350//ESTs. Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis ele-
 55 gans]//2.9e-59:474:77//Hs.125850:AA885355
 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
 F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:
 234:63//Hs.7498:U41514

F-PLACE3000362//EST//8.5e-25:302:73//Hs.140504:AA810441
 F-PLACE3000363
 F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928
 F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
 5 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
 F-PLACE3000399//Clathrin, light polypeptide (Lcb) (5.2e-70:391:81//Hs.73919:X81637
 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
 F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
 F-PLACE3000402//ESTs//2.4e-84:425:98//Hs.148962:AI219715
 10 F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:
 116.78//Hs.77579:AF013263
 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:
 H61502
 15 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:
 AB018344
 F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:
 183.93//Hs.108326:AB006202
 20 F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA81874
 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
 F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:
 AB018352
 25 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone C1T987SK-A-69G12//1.1e-06:244:63//Hs.154050:
 AC004131
 F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.
 40993:AF000148
 30 F-PLACE4000063
 F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W0073
 F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
 F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:
 35 AB007931
 F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
 F-PLACE4000129
 F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H09627
 F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
 40 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
 F-PLACE4000192
 F-PLACE4000211
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
 45 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI034317
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
 mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
 50 F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200
 F-PLACE4000261
 F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:
 100//Hs.118849:AA215645
 F-PLACE4000270
 55 F-PLACE4000300
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966
 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

F-PLACE4000344//EST//8.4e-05:135:67//Hs.146729:AI147292
 F-PLACE4000367
 F-PLACE4000369
 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
 5 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:
 AB014540
 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982
 10 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200
 F-PLACE4000445
 F-PLACE4000450
 F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874
 F-PLACE4000487//Sialophorin (gpl115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075
 15 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:RR38951
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731
 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022
 20 F-PLACE4000548
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:
 AF000986
 F-PLACE4000581
 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-
 25 13:275:68//Hs.113980:AI034080
 F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675
 F-PLACE4000612//Keratin 9/0.27:207:64//Hs.2783:Z29074
 F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:
 AB02446
 30 F-PLACE4000650
 F-PLACE4000654
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132
 F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299
 35 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688
 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:
 AB014554
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254
 F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877
 40 F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
 F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194
 F-THYRO1000034
 F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099
 F-THYRO1000040//ESTs//0.331:59//Hs.87176:AI148326
 45 F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345
 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557
 F-THYRO1000085
 F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065
 F-THYRO1000107
 50 F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//8.8e-106:690:86//Hs.23094:M19503
 F-THYRO1000121
 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732
 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:
 AF087142
 55 F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203
 F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416
 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219
 F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

- 152936:D63475
F-THYRO1000186//Homo sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312
- F-THYRO1000187//EST/0.11:227:62//Hs.101773:H23270
- F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883
- 5 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698
- F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552
- F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848
- 10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297
- F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322
- F-THYRO1000242//Zinc finger protein 84 (HPF2)/1.2e-42:534:64//Hs.9450:M27878
- F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590
- F-THYRO1000270
- 15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500
- F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068
- F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:A777803
- F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175
- 20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333
- F-THYRO1000358//Human selenium-binding protein (HSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091
- F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919
- 25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134
- F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855
- F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413
- 30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572
- F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238
- F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773
- F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115
- 35 F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520
- F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663
- F-THYRO1000488
- F-THYRO1000501//Homo sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200
- F-THYRO1000502//ESTs//1.350:57//Hs.119749:AA689298
- F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120
- 40 F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877
- F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713
- F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949
- F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587
- F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322
- F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331
- F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053
- 50 F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081
- F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941
- F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125
- F-THYRO1000658//CD4 receptor [exons 1 and 2] [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267
- F-THYRO1000662
- 55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157
- F-THYRO1000676//CD4 receptor [exons 1 and 2] [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267
- F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

F-THYRO1000699//ESTs//1.6e-10.314:65//Hs.139212:AA243452
 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
 F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06.631:59//Hs.79706:U53204
 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA808085
 5 F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871
 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:
 AF061573
 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481
 F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:
 10 452:58//Hs.11538:AF006084
 F-THYRO1000787
 F-THYRO1000793
 F-THYRO1000796
 F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:
 15 AB002446
 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087
 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
 F-THYRO1000843
 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AAB83788
 20 F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
 F-THYRO1000865//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.0e-33:
 190:75//Hs.13526:N21103
 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
 F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.
 25 92381:AB007956
 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:
 839:98//Hs.78106:AF079529
 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836
 F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263
 30 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963
 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear
 gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169
 F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
 F-THYRO1000983
 35 F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
 F-THYRO1001003
 F-THYRO1001131//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369
 F-THYRO1001033//H.sapiens mRNA for cyclin II//0.0061:287:60//Hs.3232:Z46788
 40 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830
 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353
 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-14:74:74//Hs.159249:Z99130
 F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700
 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N85416
 45 F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425
 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
 F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
 F-THYRO1001173
 F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
 50 F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
 F-THYRO1001204
 F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
 F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
 55 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:
 AF027156
 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872
 F-THYRO1001321//*Homo sapiens* DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333
 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545
 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
 5 F-THYRO1001363//ESTs//1.6e-16:178:78//Hs.163954:N57939
 F-THYRO1001365//*Homo sapiens* KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877
 F-THYRO1001374//*Homo sapiens* mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:
 AB014607
 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993
 10 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946
 F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694
 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659
 F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
 F-THYRO1001426//Human zinc finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//
 15 Hs.102877:U41315
 F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215
 F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830
 F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943
 20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
 F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
 F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
 25 F-THYRO1001573//*Homo sapiens* clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572
 F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655
 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535
 F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
 30 F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659
 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:
 M91463
 F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568
 35 F-THYRO1001671//*Homo sapiens* mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//
 Hs.118633:AJ25089
 F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238
 F-THYRO1001703//*Homo sapiens* clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552
 F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
 40 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [*Drosophila melanogaster*]//2.5e-51:296:92//
 Hs.3826:U69560
 F-THYRO100173 //EST//6.9e-30:180:94//Hs.58641:W81229
 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
 F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
 45 F-THYRO1001772//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//2.2e-21:
 182:81//Hs.118053:N75725
 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
 F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295
 F-THYRO1001828
 50 F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.
 51061:M24283
 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
 F-VESEN1000122
 55 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
 F-Y79AA1000033
 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689
 F-Y79AA1000059//*Homo sapiens* immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

U78521
F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680
F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053
F-Y79AA1000181//Fatty acid synthase (3' region) [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//
5 0.0022:684:58//Hs.83190:U29344
F-Y79AA1000202//ESTs/2.5e-17:143:86//Hs.76925:AA211860
F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds/3.9e-73:345:100//Hs.
9242:AF08192
F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079
10 F-Y79AA1000231//ESTs/0.11:209:66//Hs.132184:AI278623
F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134
F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds/9.1e-11:300:64//Hs.23311:AB002365
F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D505919
F-Y79AA1000328
15 F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:
AF071309
F-Y79AA1000346
F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853
F-Y79AA1000355
20 F-Y79AA1000368//ESTs/0.0062:235:64//Hs.114777:AA782908
F-Y79AA1000405//ESTs/0.76:244:62//Hs.153027:AA648897
F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219
F-Y79AA1000420//ESTs/1.1e-53:271:87//Hs.13056:AA181018
F-Y79AA1000469//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:
25 AF082516
F-Y79AA1000480
F-Y79AA1000538//ESTs/5.7e-09:110:77//Hs.98790:AA284871
F-Y79AA1000539//ESTs/2.6e-52:412:77//Hs.81648:W26521
F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356
30 F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:
AF068706
F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:
AF091080
35 F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:
AF060503
F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513
F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:
98/Hs.83023:AF093670
40 F-Y79AA1000748//ESTs/4.2e-12:95:90//Hs.33687:R85969
F-Y79AA1000752//ESTs/8.1e-114:551:97//Hs.153471:AI198377
F-Y79AA1000774//ESTs/2.9e-59:296:98//Hs.150536:W20067
F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:
45 AF098799
F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085
F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:
AF059569
50 F-Y79AA1000805
F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568
F-Y79AA1000827//Fatty acid synthase (3' region) [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//
0.0048:630:57//Hs.83190:U29344
F-Y79AA1000833//TUBULIN ALPHALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956
55 F-Y79AA1000850//ESTs. Weakly similar to T22C1.7 [C. elegans]//6.0e-77:368:99//Hs.86660:AA398644
F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:
D16815
F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

- F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]/6.9e-69:
310.94//Hs.76822;AI359536
- F-Y79AA1000969//LYMphotoxin-Beta RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
- F-Y79AA1000976//Arachidonate 5-lipoxygenase//0.87:174:66//Hs.73809:M23892
- 5 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
- F-Y79AA1001023
- F-Y79AA1001041//Human mytY homolog (MYTH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
- F-Y79AA1001061//ESTs/3.6e-41:303:84//Hs.55855;AA621381
- 10 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157670:AI357511
- F-Y79AA1001077//ESTs/4.9e-40:237:94//Hs.11197:AA309047
- F-Y79AA1001078
- F-Y79AA100105//*Homo sapiens* homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967;AF022654
- 15 F-Y79AA1001145//ESTs/1.3e-20:234:75//Hs.55855;AA621381
- F-Y79AA1001167//*Homo sapiens* mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
- F-Y79AA1001177//Human sHIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
- F-Y79AA1001185//ESTs/1.7e-56:318:93//Hs.102991:AA639646
- F-Y79AA1001211//ESTs/9.1e-108:503:99//Hs.100605:AA305965
- 20 F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
- F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
- F-Y79AA1001233//ESTRADOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
- F-Y79AA1001236//*Homo sapiens* mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc101I13Q7 (R2PD Berlin))//4.0e-135:44.1:97//Hs.23170:AJ005892
- 25 F-Y79AA1001281//ESTs/2.7e-21:157:88//Hs.163825:AI393240
- F-Y79AA1001299//Human In1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
- F-Y79AA1001312//ESTs/3.7e-95:448:99//Hs.104469:W38395
- F-Y79AA1001323//ESTs/8.9e-50:340:86//Hs.144198:AI017555
- F-Y79AA1001384
- 30 F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
- F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [*C.elegans*]/1.5e-90:424:96//Hs.154221:H23167
- F-Y79AA1001402//ESTs/1.0:245:62//Hs.134695:AI088489
- F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
- F-Y79AA1001511//ESTs/9.9e-105:487:99//Hs.153581:AA630465
- 35 F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [*Homo sapiens*]//0.95:
256.63//Hs.29974:AI360447
- F-Y79AA1001541//EST//0.9.6.202:61//Hs.99141:AA447744
- F-Y79AA1001548//ESTs/2.6e-25:166:90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs/1.6e-35:191:97//Hs.52885:H29851
- 40 F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
- F-Y79AA1001585//ESTs/1.1e-84:473:93//Hs.42547:AA210783
- F-Y79AA1001594//ESTs/1.7e-08:169:71//Hs.97366:AA393109
- F-Y79AA1001603//ESTs/4.6e-07:429:59//Hs.160422:AI363426
- F-Y79AA1001613//*Homo sapiens* mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:
45 AB014583
- F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [*C.elegans*]//9.4e-79:421:94//Hs.107039:W27244
- F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
- F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:
X04526
- 50 F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
- F-Y79AA1001696//ESTs/2.3e-44:249:94//Hs.163665:AA250877
- F-Y79AA1001705//*Homo sapiens* interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:
609.58//Hs.77297:L77619
- F-Y79AA1001711//ESTs/5.2e-29:224:83//Hs.100461:AI018620
- 55 F-Y79AA1001781//*Homo sapiens* KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
- F-Y79AA1001805//ESTs/1.1e-62:315:98//Hs.16141:W56079
- F-Y79AA1001827//ESTs, Weakly similar to Similar to *S.cerevisiae* YD9335.03c protein [*H.sapiens*]//2.9e-62:313:
98//Hs.15709:W81213

F-Y79AA1001846//ESTs/9.4e-16:146:82//Hs.140588:H60533
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]/1.6e-19:142:90//Hs.103349:AI141124
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10/5.1e-09:215:67//Hs.104115:X52332
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds/5.4e-06:412:62//Hs.106387:AF029778
 5 F-Y79AA1001875//ESTs/6.8e-09:198:67//Hs.138036:AI343173
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds/0.98:430:58//Hs.
 785011:L13720
 F-Y79AA1001963//ESTs/8.1e-131:642:97//Hs.54971:AI424382
 F-Y79AA1002027//ESTs/0.00042:58:91//Hs.5375:AA620611
 10 F-Y79AA1002083//ESTs/2.5e-51:285:95//Hs.117205:W88943
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]///8.3e-53:348:88//Hs.18122:AI338045
 F-Y79AA1002093
 F-Y79AA1002103//ESTs/1.5e-15:223:71//Hs.97427:AA411865
 F-Y79AA1002115
 15 F-Y79AA1002125//ESTs/6.5e-41:206:99//Hs.159257:N40395
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]/1.2e-24:165:90//Hs.6473:AA853955
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds/9.5e-05:393:62//Hs.77864:AB014538
 F-Y79AA1002208//ESTs/2.7e-13:211:69//Hs.112469:AA598515
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldothermophilus]/2.3e-113:568:
 20 96//Hs.111637:AA305890
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]///8.6e-33:338:73//Hs.26662:U55984
 F-Y79AA1002211//ESTs/2.6e-15:121:75//Hs.159584:AA524477
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds/4.1e-176:821:98//Hs.100729:
 AB014592
 F-Y79AA1002246//Human involucrin mRNA/5.6e-05:525:59//Hs.157091:M13903
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:
 AB014555
 30 F-Y79AA1002298//ESTs/2.5e-05:115:77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:
 AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete
 35 cds//0.028:587:58//Hs.2363:L36069
 F-Y79AA1002361//ESTs/8.7e-29:149:100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs/1.5e-25:183:89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase/9.1e-51:489:72//Hs.84112:X52142
 40 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302
 45 Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

- the name of clone,
 title of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.
- [0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.
 [0313] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA100005//ESTs, Highly similar to HYPOTHETICAL 31.16 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]/5.6e-93.501.93/Hs.13015-AA628434
 R-HEMBA100030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233
 R-HEMBA100042//Archain//1.4e-45.282:89//Hs.33642-X81198
 5 R-HEMBA100046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087
 R-HEMBA100050//EST//0.043:155:63/Hs.149031:AI243340
 R-HEMBA100076//ESTs//3.1e-77.394:97//Hs.111742:R39329
 R-HEMBA100111//ESTs//1.7e-33.228:85//Hs.146811:AA410788
 R-HEMBA100129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]/4.4e-90.502:90//Hs.
 10 55918:AA151667
 R-HEMBA100141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100.514:94//Hs.27197:
 AB018340
 R-HEMBA100150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45.435:77//Hs.153026:
 AB014540
 15 R-nnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]/7.7e-92.428:
 100//Hs.126925-AA931237
 R-HEMBA100158
 R-nnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]/1.3e-05.58:91//Hs.5570:AI377863
 R-HEMBA100180//ESTs//7.7e-90.461:95//Hs.159200:N50545
 20 R-HEMBA100185//ESTs//1.3e-72.371:96//Hs.134506-AA308366
 R-HEMBA100193//ESTs//4.2e-103.481:99//Hs.143251:AA769927
 R-HEMBA100201//Human lnl1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847
 R-HEMBA100213//ESTs//5.4e-85.465:94//Hs.23412:AA133311
 R-HEMBA100216//ESTs//3.0e-37.311:79//Hs.137875:AA993532
 25 R-nnnnnnnnnnn//EST//2.2e-100.498:96//Hs.161570:W80404
 R-HEMBA100231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874
 R-HEMBA100243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:
 AB007944
 R-HEMBA100244//ESTs//2.3e-88.455:96//Hs.8929:AA719019
 30 R-HEMBA100251//ESTs//0.96:411:56//Hs.120277:AI243808
 R-HEMBA100264//ESTs//3.7e-97.487:96//Hs.29258:W37424
 R-nnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]/4.9e-14.208:73//Hs.93332:
 AA811920
 R-HEMBA100282//ESTs//2.5e-38.216:94//Hs.120757:R92485
 35 R-HEMBA100288//ESTs//2.6e-43.289:86//Hs.151365-AA643962
 R-HEMBA100290//ESTs//5.1e-110.543:96//Hs.139068:AA516409
 R-HEMBA100302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099
 R-nnnnnnnnnnnn//ESTs//7.4e-76.386:97//Hs.22276:AA191323
 R-nnnnnnnnnnnn//Human Ca²⁺-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//
 40 Hs.151301:U36448
 R-HEMBA100307//ESTs, Highly similar to 8A-2V protein [M.musculus]/1.1e-103:489:99//Hs.108881:AI018024
 R-nnnnnnnnnnnn//ESTs//9.99:47:92:98//Hs.163512-AA903238
 R-HEMBA100338//EST//5.1e-49.278:92//Hs.150815:AI302560
 R-HEMBA100351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//
 45 Hs.73614-U83460
 R-HEMBA100355//ESTs//1.0e-105.531:96//Hs.61762:AI222243
 R-HEMBA100357//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:
 K00629
 R-HEMBA100366//ESTs//1.1e-99.524:95//Hs.11785:T65857
 50 R-HEMBA100369//ESTs//6.5e-70.355:96//Hs.124847:AA843938
 R-HEMBA100376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960
 R-HEMBA100387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//
 Hs.73614-U83460
 R-HEMBA100390//Oxytocin receptor//2.4e-16.428:62//Hs.2820:X64878
 55 R-HEMBA100392//ESTs//3.9e-105.531:96//Hs.130661:AI340248
 R-HEMBA100396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]/1.1e-44.447:75//Hs.42849:N31920
 R-HEMBA1004011//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]/6.1e-92.373:99//Hs.48675:
 AI005282

- R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
 R-HEMBA1000428//Homo sapiens mRNA for oligoprenin 1//4.9e-85:535:87//Hs.158122:AJ001189
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
 5 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
 R-HEMBA1000460
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
 10 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219
 R-HEMBA1000488//ESTs, Weakly similar to Th KIAA0132 gene product is related to Drosophila melanogaster ring canel protein [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449
 R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
 15 R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
 R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
 R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
 20 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:
 U15782
 R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.
 99722:AI422277
 25 R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317
 R-nnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
 R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:
 30 W74481
 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
 R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
 R-nnnnnnnnnnnn
 R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
 35 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
 R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:
 AJ007509
 R-HEMBA1000592//TYROSINE-PROTEIN KINASE
 ITK/TSK//0.024:309:61//Hs.89519:L10717
 40 R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.
 158334:U86136
 R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
 45 R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:
 AA643235
 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:
 AB014590
 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390
 50 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
 R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922
 R-HEMBA1000682//ESTs, Weakly similar to putative pl 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
 R-HEMBA1000686//ESTs, Weakly similar to C2F7.2 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:
 AI141736
 R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:
 AF057280
 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

R-HEMBA1000719//ESTs//8.4e-90:484.94//Hs.29005:AA477213
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:
572.95//Hs.28644:AI018612
R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449.75//Hs.74478:
U33931
R-HEMBA1000727//ESTs//0.0047:267.60//Hs.133095:AA927777
R-HEMBA1000747//EST//3.9e-20:160.85//Hs.99048:AA446110
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)/(4.7e-37:286.82//Hs.155464:AF088219
R-HEMBA1000752//EST//0.041:39.94//Hs.122772:AA961131
10 R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309.75//Hs.
10458:AF088219
R-HEMBA1000773//EST//7.5e-05:201.63//Hs.122887:AA767612
R-HEMBA1000774//Kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen, (R2 leukocyte antigen,
antigen detected by monoclonal and antibody IA4))//1.3e-48:284.90//Hs.103458:X53795
15 R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291.87//Hs.154326:D42087
R-HEMBA1000817//ESTs//8.3e-95:445.99//Hs.107357:AA983939
R-HEMBA1000822//ESTs//1.1e-107:522.97//Hs.92832:AA631027
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-
44:228.98//Hs.18192:AF048977
20 R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410.77//Hs.154103:AF061258
R-HEMBA1000851
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284.80//Hs.159608:
U46689
R-HEMBA1000867//EST//2.0e-17:211.74//Hs.145670:AI265794
25 R-HEMBA1000869//ESTs//3.1e-16:237.71//Hs.116518:AA653202
R-HEMBA1000870//ESTs//1.6e-43:222.98//Hs.69564:AA203608
R-HEMBA1000872//ESTs//1.9e-93:453.98//Hs.152622:AA594951
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)/(3.0e-41:329.79//Hs.155464:AF088219
R-HEMBA1000908//ESTs//1.6e-51:291.92//Hs.12247:AI203154
30 R-HEMBA1000910//EST//0.98:139.64//Hs.132687:AI033672
R-HEMBA1000918//EST//9.6e-30:152.84//Hs.162136:AA526508
R-HEMBA1000919
R-HEMBA1000934//ESTs//4.1e-38:254.89//Hs.87784:AA460597
R-HEMBA1000942//ESTs//3.5e-20:172.69//Hs.160065:AI018619
35 R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281.78//Hs.33187:
AB018291
R-HEMBA1000946//ESTs//1.6e-68:352.96//Hs.21331:H93074
R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347.81//Hs.5247:AF029750
R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362.84//Hs.
40 159187:AB007977
R-HEMBA1000971//ESTs//2.8e-41:246.91//Hs.104287:AI363498
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341.81//Hs.44766:AJ007590
R-HEMBA1000974//ESTs//1.4e-32:166.100//Hs.149274:AI018170
R-HEMBA1000975//Oxytocin receptor//2.7e-46:563.73//Hs.2820:X64878
45 R-HEMBA1000985//ESTs//4.4e-05:125.69//Hs.147434:AI214464
R-HEMBA1000986//ESTs//7.8e-44:266.84//Hs.163784:N54902
R-HEMBA1000991//EST//1.4e-42:162.86//Hs.149580:AI281881
R-HEMBA1001007
R-HEMBA1001008//ESTs//2.3e-82:463.92//Hs.10339:AA058764
50 R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:
100//Hs.128738:AA970836
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587.95//Hs.158287:
AB007937
R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140.95//Hs.58393:X05360
55 R-HEMBA1001020//ESTs//0.52:86.72//Hs.69683:AA115292
R-HEMBA1001022//ESTs//3.4e-18:102.100//Hs.63243:AI123912
R-HEMBA1001024//ESTs//1.9e-07:262.61//Hs.124399:AA832336
R-HEMBA1001026//ESTs//0.0017:142.67//Hs.144109:AI345543

R-nnnnnnnnnn/Ankyrin G/0.23:244:60//Hs.75893:U13618
 R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:
 AB014521
 R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886
 5 R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813
 R-HEMBA1001071//Alpha-1 type 3 collagen/9.1e-34:179:98//Hs.119571:X14420
 R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.
 127338:AB007961
 R-HEMBA1001080
 10 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788
 R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674
 R-HEMBA1001094
 R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245
 R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219
 15 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974
 R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320
 R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530
 R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341
 R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265
 20 R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219
 R-HEMBA1001172//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.1e-
 39:309:82//Hs.96337:AA225358
 R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:
 AB007961
 25 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896
 R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:
 62//Hs.100238:U69194
 R-HEMBA1001226//Homo sapiens PYRN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
 30 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435
 R-nnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
 35 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
 R-HEMBA1001303//EST//0.0053:271:60//Hs.156148:AI333214
 40 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AB206019
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC
 REGION [S.cerevisiae]//1.17162:AA701259
 45 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
 R-HEMBA1001330//Homo sapiens PYRN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
 R-HEMBA1001361//ESTs//3.5e-107:57:94//Hs.7727:AA142837
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
 50 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204
 55 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714
 R-HEMBA1001407//ESTs//2.7e-76:365:99//Hs.110128:AA584364
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199
 R-HEMBA1001415
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981
 R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704
 5 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263
 R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982
 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546
 R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077
 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503
 10 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220
 R-HEMBA1001463
 R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008
 R-HEMBA1001478
 R-HEMBA1001497
 15 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426
 R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503
 R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269
 R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493
 R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:NG64723
 20 R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270
 R-HEMBA1001557//ESTs//2.e-83:413:97//Hs.47546:AA181348
 R-HEMBA1001566//Small inducible cytokine A5 (RANTES)/(3.4e-50:304:88//Hs.155464:AF088219
 R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324
 R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880
 25 R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030
 R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652
 R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329
 R-HEMBA1001589
 R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874
 30 R-HEMBA1001608//Human kpn1 repeat mma (cdna clone pcd-kpn1-8), 3' end//1.3e-73:533:82//Hs.103948:K00627
 R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]
 //4.5e-93:537:90//Hs.20218:AA628530
 R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694
 35 R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158
 R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623
 R-nnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398
 R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554
 R-HEMBA1001658
 40 R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:
 AF029343
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:
 92//Hs.107254:AC005943
 R-HEMBA1001675
 45 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:
 94//Hs.7381:AF038962
 R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424
 R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:
 50 AB014598
 R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960
 R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095
 R-HEMBA1001714//ESTs, Highly similar to ATMPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-
 vegicus]//1.8e-46:236:98//Hs.132948:AA194452
 55 R-HEMBA1001718//Small inducible cytokine A5 (RANTES)/(8.6e-43:166:88//Hs.155464:AF088219
 R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN
 SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105
 R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39.366.77//Hs.153014:AB002353
R-HEMBA1001744
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162
5 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243
10 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823
R-nnnnnnnnnnnn/Zinc finger protein 148 (pHZ-52)/0.78:232:57//Hs.112180:AF039019
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.
118164:AB007969
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334
15 R-HEMBA1001810//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179
R-HEMBA1001819//ZINC FINGER PROTEIN HF 12//1.2e-16:259:69//Hs.155470:X07290
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707
R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210
20 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:
AB014517
25 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein (alternative products)//1.9e-37:357:76//Hs.53217:
Z48051
R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.
9489:R84329
30 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128
R-HEMBA1001910
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:
347:100//Hs.30991:AA994438
35 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.
91251:U66685
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:
40 534:96//Hs.154934:AF000145
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-
99:482:98//Hs.96849:AA879470
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI027122
45 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:T0048
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825
50 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/
Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains
a putative CpG Island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA93932
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
55 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550
 R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
 R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312
 R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:
 5 AB011135
 R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
 R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
 R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
 R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369
 10 R-HEMBA1002113//Prostaglandin D2 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402
 R-HEMBA1002119//Homo sapiens EST/E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:
 AF065854
 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868
 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957
 15 R-HEMBA1002144//ESTs//3.1e-30:259:77//Hs.141575:AA211734
 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
 R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
 R-HEMBA1002160//Homo sapiens nephrocytins (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:
 20 AF023674
 R-HEMBA1002161//Homo sapiens EV15 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
 R-HEMBA1002166//Thromboxane A2 receptor//8.8e-46:296:81//Hs.89887:D38081
 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
 25 R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete
cds//6.0e-42:419:73//Hs.159523:AF001622
 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:
 AB007958
 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
 30 R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
 R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
 R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:
 35 AB014606
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//
 Hs.25664:AF089814
 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
 R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
 40 R-HEMBA1002257
 R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL_27.8_KD_PROTEIN_IN_VMA7-RPS31A_INTERGEN-
 IC_REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
 R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
 45 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818
 R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:
 AB018314
 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04282
 50 R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
 R-nnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:
 661:93//Hs.119023:AF092563
 R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
 R-HEMBA1002386//EST//2.3e-05:132:69//Hs.37558:H58237
 55 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849
 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267
 R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

R-HEMBA1002458//ESTs//1.8e-88:448.95//Hs.97914-AA769069
 R-HEMBA1002460//Catalase//0.67:314.60//Hs.76359-X04085
 R-HEMBA1002462//EST//0.032:44.88//Hs.161536:N80395
 R-nnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488.95//Hs.108115.AA582193
 5 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281.80//Hs.43681:AL022394
 R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311.88//Hs.155464:AF088219
 R-HEMBA1002495//ESTs//1.2e-94:457.98//Hs.42140:AI188995
 R-HEMBA1002498//ESTs//1.7e-35:240.78//Hs.119871:AA705133
 R-HEMBA1002503//ESTs//2.3e-14:64.85//Hs.140190:AA701449
 10 R-HEMBA1002508//ESTs//0.00057:160.62//Hs.149661:AA872990
 R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21) //2.3e-113:456.92//Hs.6764:
 AJ011972
 R-HEMBA1002515//EST//1.0:153.63//Hs.118045:N51715
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564.93//Hs.129928:
 15 AB007923
 R-HEMBA1002542//ESTs//1.0e-101:539.93//Hs.93872:AA524700
 R-HEMBA1002547//EST//8.7e-27:151.96//Hs.132145:AI041804
 R-HEMBA1002552//EST//5.9e-49:335.85//Hs.149580:AI281881
 R-HEMBA1002555//ESTs//1.1e-77:461.91//Hs.38750:N30012
 20 R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264.89//Hs.32567:AF073519
 R-HEMBA1002561//Small inducible cytokine A5 (RANTES) //6.4e-40:196.78//Hs.155464:AF088219
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587.97//Hs.151411:
 AF075587
 R-HEMBA1002583//ESTs//7.1e-79:410.95//Hs.21599-AA478904
 25 R-HEMBA1002590//EST//3.3e-54:278.97//Hs.138637:N20838
 R-HEMBA1002592//ESTs//2.6e-44:500.74//Hs.110934:N26055
 R-HEMBA1002621
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380.97//Hs.91338:
 AB018351
 30 R-HEMBA1002628//ESTs//0.0020:167.66//Hs.140605:AA830881
 R-HEMBA1002629//ESTs//0.00014:50.100//Hs.119132:AA398715
 R-HEMBA1002645//EST//2.1e-37:285.82//Hs.141728:W73041
 R-HEMBA1002651//EST//2.2e-23:374.69//Hs.139357:AA420970
 R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA, com-
 35 plete cds//1.5e-53:406.81//Hs.108966:U48696
 R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296.84//Hs.6232:
 AB018307
 R-HEMBA1002666//EST//4.4e-09:79.88//Hs.72015:AA151945
 R-HEMBA1002678//EST, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-
 40 104:560.92//Hs.161748:T64896
 R-nnnnnnnnnnnn//EST//0.15:136.69//Hs.129570:AA995396
 R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247.62//Hs.142023:M88282
 R-HEMBA1002696//ESTs//3.5e-94:529.92//Hs.16725:AA196477
 R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302.86//Hs.15519:
 45 AB018315
 R-HEMBA1002716//ESTs//1.3e-109:555.96//Hs.9812:AA147884
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287.81//Hs.132942:
 AB014521
 R-HEMBA1002730//ESTs//1.2e-95:488.95//Hs.22030:AA521168
 50 R-HEMBA1002742//ESTs//1.0e-91:437.99//Hs.139987:AA652163
 R-HEMBA1002746//ESTs//4.4e-97:468.98//Hs.129903:AA576526
 R-HEMBA1002748//ESTs//5.0e-98:475.98//Hs.125461:AI375792
 R-HEMBA1002750//ESTs//1.6e-42:223.97//Hs.40460:N36090
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545.95//Hs.74750:
 55 AB011126
 R-HEMBA1002770//EST//0.34:294.59//Hs.43091:N22127
 R-HEMBA1002777//ESTs//3.0e-85:316.98//Hs.17537:C06491
 R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342.58//Hs.48824:D87717

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333
 R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709
 R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA0913320
 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:
 5 AF071185
 R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204
 R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013
 R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.
 5337:AA243757
 10 R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514
 R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830
 R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:A1220827
 R-HEMBA1002886//EST//3.2e-85:401:99//Hs.98580:AA405670
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//
 15 Hs.33787:AF037261
 R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
 R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
 R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
 R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
 20 R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165
 R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
 R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
 R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:A1190892
 R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
 25 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
 R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405
 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
 R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
 R-nnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064
 30 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:
 96//Hs.125749:AI377682
 R-HEMBA1003021//Homo sapiens PYRN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080
 R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
 R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577
 35 R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
 R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366
 R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN
 CHROMOSOME 1 PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442
 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-
 40 119:578:97//Hs.44097:AF054182
 R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
 R-HEMBA1003067//Van Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238
 R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903
 R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235
 45 R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
 R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249
 R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219
 R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
 R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//
 50 Hs.104800:AA709155
 R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
 R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058
 R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.
 118717:U86751
 55 R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370485
 R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615
 R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

- R-HEMBA1003148//Homo sapiens mRNA for dachshund protein 3/3.6e-118:586:96//Hs.63931:AJ005670
 R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
 R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
 5 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804
 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:
 AB014540
 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
 R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265
 10 R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR
 [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817
 R-HEMBA1003227//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:
 W27666
 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
 15 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.
 152663:AF068864
 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219
 20 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392
 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785
 R-HEMBA1003281
 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:
 AB011109
 25 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.
 124224:AB001872
 30 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:
 AF026029
 35 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
 40 R-HEMBA1003380//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.8e-
 11:261:65//Hs.87578:AI125363
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
 R-HEMBA1003395//ESTs//5.2e-14:108:89//Hs.162208:AA536127
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424-AA774204
 45 R-nnnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309
 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121
 50 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
 55 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.
 91619:AA552351

R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058
 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.
 5 58598:AA625440
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
 R-HEMBA1003579//EST//0.0057:239:60//Hs.162828:AA643892
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
 10 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
 R-HEMBA1003615
 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
 15 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
 R-HEMBA1003622//EST//1.1e-46:488:75//Hs.139093:AA166888
 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
 R-HEMBA1003637//ESTs, Weakly similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! [H.sapiens]//9.3e-24:
 189.84//Hs.142208:AA209438
 20 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.995395:R59010
 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.
 67619:AB007957
 25 R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635
 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.
 9489:R84329
 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
 30 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.
 22934:AA581379
 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
 R-HEMBA1003692//Human cytochrome P450-1IB (h1IB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:
 M29873
 35 R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064
 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.
 1139:X77777
 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.2e-
 40 33:377:74//Hs.24040:AF006823
 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122584:AA778847
 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258393
 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040
 45 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT
 [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
 50 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868
 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
 55 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219
 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium
 tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

R-HEMBA1003856//ESTs//8.2e-20:266.71//Hs.48312:N68161
 R-HEMBA1003864//ESTs//1.6e-99:528.93//Hs.26890:AA449033
 R-HEMBA1003866//POLYPOSI S LOCUS PROTEIN I//0.30:146.64//Hs.74648:M73547
 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-58:295.98//Hs.161661:AA166911
 R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286.79//Hs.61408:AF070621
 R-HEMBA1003885//ESTs//4.6e-50:293.90//Hs.142314:AA347930
 R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294.86//Hs.13572:AF068179
 R-HEMBA1003902//ESTs//1.8e-43:300.85//Hs.146811:AA410788
 R-HEMBA1003908//ESTs//3.5e-91:477.94//Hs.6638:AA536187
 R-HEMBA1003926//ESTs//7.9e-44:294.87//Hs.164036:AA845659
 R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276.81//Hs.72660:AB011157
 R-HEMBA1003939
 R-HEMBA1003942//ESTs//1.6e-81:428.94//Hs.50418:AA524669
 R-HEMBA1003950//ESTs//8.1e-54:283.95//Hs.145528:AA261545
 R-HEMBA1003953//ESTs//3.8e-30:194.89//Hs.99681:AA504591
 R-HEMBA1003958//ESTs//4.0e-45:394.77//Hs.141602:N63562
 R-HEMBA1003959//ESTs//5.2e-28:197.86//Hs.9951:W56253
 R-HEMBA1003976//ESTs//2.0e-29:232.84//Hs.133947:A074525
 R-HEMBA1003978//ESTs//3.2e-115:549.98//Hs.76798:AI050882
 R-HEMBA1003985//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//2.2e-91:
 448.97//Hs.117834:AA766771
 R-HEMBA1003987//ESTs//8.1e-36:193.88//Hs.151844:N92756
 R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360.81//Hs.150275:D87682
 R-HEMBA1004000//EST//5.5e-62:308.97//Hs.50438:N74105
 R-HEMBA1004011//ESTs//8.6e-85:431.96//Hs.36185:R99899
 R-HEMBA1004012//ESTs//1.3e-40:309.83//Hs.140329:AA714011
 R-HEMBA1004015//ESTs//5.1e-97:453.99//Hs.111446:AI333774
 R-HEMBA1004024//ESTs//5.2e-19:159.79//Hs.138856:H47461
 R-HEMBA1004038//ESTs//1.3e-41:346.79//Hs.146173:AA906191
 R-HEMBA1004042//ESTs//0.0012:201.69//Hs.24248:AA528253
 R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365.70//Hs.99692:AA811804
 R-HEMBA1004048//ESTs//9.5e-104:497.98//Hs.77735:AI25469
 R-HEMBA1004049//HEAT SHOCK 70 KU PROTEIN 1//6.3e-31:176.96//Hs.8997:M11717
 R-HEMBA1004055//ESTs//1.7e-115:577.96//Hs.59503:W63754
 R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577.82//Hs.113283:AF018080
 R-HEMBA1004074//EST//1.0:152.61//Hs.149093:AI243988
 R-HEMBA1004086//ESTs//4.0e-53:266.98//Hs.34658:N98652
 R-HEMBA1004097//ESTs//4.4e-46:279.91//Hs.110533:H16251
 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534.69//Hs.90998:D50918
 R-HEMBA1004132//ESTs//4.6e-47:316.86//Hs.141602:N63562
 R-HEMBA1004133
 R-HEMBA1004138//EST//1.7e-08:211.64//Hs.129189:AA988736
 R-HEMBA1004143//ESTs//4.0e-25:137.97//Hs.21307:AA203320
 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191.86//Hs.155464:AF088219
 R-HEMBA1004150//GRANCALCIN//0.99:357.59//Hs.79381:M81637
 R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313.84//Hs.154326:D42087
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563.96//Hs.59988:AF067855
 R-HEMBA1004199
 R-HEMBA1004200//EST//3.1e-89:441.97//Hs.141173:R97701
 R-HEMBA1004202//ESTs, Weakly similar to CTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552.94//Hs.
 10092:AI189282
 R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275.98//Hs.15832:
 AB014518
 R-HEMBA1004207//Leptin receptor//1.1e-117:573.97//Hs.54515:U50748
 R-HEMBA1004225//EST//9.7e-34:186.95//Hs.137567:R20617
 R-HEMBA1004227//ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//4.0e-
 16:117:91//Hs.92033:AA255832

R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338.83//Hs.153014:AB002353
R-HEMBA1004241//ESTs//1.3e-10:93.87//Hs.137511:AA456389
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511.72//Hs.154103:AF061258
R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221.86//Hs.7089:W37284
R-HEMBA1004264//ESTs//1.5e-80:425.95//Hs.107206:AA234962
R-HEMBA1004267//ESTs, Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]//1.4e-89:465.95//Hs.113660:D20018
R-HEMBA1004272//ESTs//4.5e-111:577.94//Hs.115696:N57931
R-nnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553.96//Hs.93677:AF091081
R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559.89//Hs.28298:AA203228
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101768:AF022795
R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223.75//Hs.81884:U13061
R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.6e-93:496.94//Hs.14337:AA534961
R-HEMBA1004306//ESTs//3.4e-26:363.68//Hs.70279:AA757426
R-HEMBA1004312//ESTs//4.8e-64:351.94//Hs.138611:HH2679
R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415.64//Hs.51199:X16281
R-HEMBA1004323//ESTs//2.1e-40:280.70//Hs.153300:AA928904
R-HEMBA1004327//ESTs//3.8e-72:343.99//Hs.151708:AA554714
R-HEMBA1004330//ESTs//4.0e-52:270.97//Hs.24654:AA456561
R-HEMBA1004334//ESTs//1.6e-46:234.98//Hs.47159:AI310231
R-HEMBA1004335//ESTs//1.9e-25:250.76//Hs.155880:AA703336
R-HEMBA1004341//ESTs//3.7e-101:480.98//Hs.69321:AA633240
R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444.90//Hs.80868:
D89667
R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286.83//Hs.153014:AB002353
R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576.93//Hs.55458:X77494
R-HEMBA1004366//ESTs//2.3e-94:524.91//Hs.111496:AA652869
R-HEMBA1004372//EST//0.27:198.60//Hs.162665:AA605057
R-HEMBA1004389//ESTs//4.1e-102:490.98//Hs.153708:AA687264
R-HEMBA1004394//ESTs//1.5e-94:471.96//Hs.151647:AA002084
R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//2.6e-41:285.83//Hs.155464:AF088219
R-HEMBA1004405//ESTs//2.0e-44:329.83//Hs.136839:H03717
R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420.99//Hs.88365:
AA648933
R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552.96//Hs.
12940:AI123518
R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463.68//Hs.23094:M19503
R-HEMBA1004460//ESTs//2.0e-104:574.93//Hs.46848:AA195829
R-HEMBA1004461//ESTs//2.9e-102:503.98//Hs.16370:AA017033
R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310.75//Hs.116549:AL009172
R-HEMBA1004482//ESTs//9.1e-05:322.62//Hs.34489:AA759306
R-HEMBA1004502//ESTs//6.9e-112:566.96//Hs.93985:N50034
R-HEMBA1004506//EST//5.3e-59:456.80//Hs.72412:AA160941
R-HEMBA1004507
R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-
GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262.99//Hs.12820:AA004271
R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:
281.89//Hs.58414:AA196947
R-HEMBA1004538//EST//3.3e-15:270.71//Hs.136667:AA707972
R-HEMBA1004554
R-HEMBA1004560//ESTs//8.2e-25:179.88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]/|1.0.305.60//Hs.30272:AA134913
 R-HEMBA1004577//ESTs//7.9e-50:319.89//Hs.22660:AA582243
 R-HEMBA1004586//ESTs//2.6e-73:384.96//Hs.9582:R39769
 R-nnnnnnnnnnnn//ESTs//6.0e-22:190.82//Hs.42530:N41661
 5 R-HEMBA1004610//ESTs//1.2e-91:438.98//Hs.47823:AA780767
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327.85//Hs.
 159897:AB007970
 R-HEMBA1004629//ESTs//2.3e-19:215.76//Hs.111995:AI375915
 R-HEMBA1004631//ESTs//3.6e-99:470.98//Hs.49303:AA810785
 10 R-HEMBA1004632//ESTs//1.0:128.66//Hs.159182:AA831152
 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III
 [Caenorhabditis elegans]//4.8e-111:532.98//Hs.12263:AA282393
 R-HEMBA1004638//ESTs//1.2e-66:341.95//Hs.122687:AI278454
 R-HEMBA1004666//ESTs//2.1e-65:333.96//Hs.98873:AA625442
 15 R-HEMBA1004669//ESTs//0.00039:116.74//Hs.138725:N76348
 R-HEMBA1004670//ESTs//1.7e-16:116.89//Hs.56825:AI057560
 R-HEMBA1004672//EST//6.7e-76:315.97//Hs.20821:R19368
 R-HEMBA1004693//ESTs//6.4e-68:327.99//Hs.159066:AI093252
 R-HEMBA1004697//ESTs//9.3e-98:467.98//Hs.62637:AA043562
 20 R-HEMBA1004705//EST//0.0034:271.58//Hs.112503:AA599042
 R-HEMBA1004709//EST//1.3e-55:392.85//Hs.149580:AI281881
 R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449.76//Hs.155464:AF088219
 R-HEMBA1004725//EST//1.8e-71:424.88//Hs.155712:AI309235
 R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467.73//Hs.91916:AF035317
 25 R-HEMBA1004733//EST//0.99:84.65//Hs.161372:AI423151
 R-HEMBA1004734//ESTs//1.8e-82:421.96//Hs.21275:N73275
 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:
 82//Hs.51187:UB228
 R-HEMBA1004748//ESTs//1.7e-43:166.86//Hs.37573:H59651
 30 R-HEMBA1004751//ESTs//8.0e-23:155.88//Hs.149464:AI279428
 R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281.89//Hs.89887:D38081
 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475.84//Hs.8102:L06498
 R-HEMBA1004756//ESTs//2.0e-81:384.99//Hs.129545:N68679
 R-HEMBA1004758//EST//2.0e-43:367.80//Hs.133006:AI049504
 35 R-HEMBA1004763//ESTs//2.0e-10:567.94//Hs.3757:W87380
 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//
 1.4e-47:379.81//Hs.141273:H66705
 R-HEMBA1004770//ESTs//0.0014:246.61//Hs.124857:AA687092
 R-HEMBA1004771//ESTs//1.1e-12:323.63//Hs.124146:AA699633
 40 R-HEMBA1004776//ESTs//2.5e-112:567.95//Hs.12680:W74476
 R-HEMBA1004778//ESTs//1.4e-33:272.75//Hs.141123:AA848167
 R-nnnnnnnnnnn
 R-HEMBA1004803//ESTs//1.0e-48:319.86//Hs.139231:W87732
 R-HEMBA1004806
 45 R-HEMBA1004807//ESTs//6.2e-77:362.100//Hs.140945:N47676
 R-HEMBA1004816//EST//4.3e-18:246.72//Hs.150552:AI053784
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141.85//Hs.80510:
 M74002
 R-HEMBA1004847
 50 R-HEMBA1004850//ESTs//1.2e-83:395.99//Hs.30925:AA577120
 R-HEMBA1004863//ESTs//7.5e-21:204.79//Hs.35036:H95267
 R-HEMBA1004864
 R-HEMBA1004865//EST//6.7e-18:191.75//Hs.129944:AA429362
 R-HEMBA1004880//EST//4.4e-70:346.98//Hs.145094:AA452409
 55 R-HEMBA1004889//ESTs//4.8e-117:496.97//Hs.15641:W63676
 R-HEMBA1004900//ESTs//1.2e-15:283.68//Hs.157606:AI357470
 R-HEMBA1004909//ESTs//7.3e-44:366.79//Hs.140329:AA714011
 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313.89//Hs.40100:AB002390

- R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388
 R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053
 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:
 80//Hs.1361:M55053
- 5 R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883
 R-HEMBA1004934//ESTs//1.3e-103:522:98//Hs.40415:AA037215
 R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434
 R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007
 R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
- 10 R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040
 R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035
 R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065
 R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404
 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.
 129734:AJ001683
- 15 R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329
 R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894
 R-HEMBA1004995
 R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
- 20 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212
 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:
 AB014548
- R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
 8.4e-95:491:94//Hs.16085:AI261382
- 25 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067
 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348
 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//
 Hs.16258:AI376436
- 30 R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
 R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905
 R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789
- 35 R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077
 R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
 R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:
 AF080561
- R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
 R-HEMBA1005123//Ley I//3.6e-58:519:77//Hs.37062:AC005952
- 40 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.
 67819:AB007957
- R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:
 AF039694
- 45 R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
 R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
- R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239
- 50 R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:
 61//Hs.26931:AF061836
- R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284
- 55 R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687
 R-HEMBA1005241//ESTs//3.6e-113:564:98//Hs.12770:WB4331
 R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834
 R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896
- R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157
- R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862
- R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391
- R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

R-HEMBA1005296//ESTs//4.3e-33:188:100//Hs.13916:AI025750
 R-HEMBA1005304//SmaI inducible cytokine A5 (RANTES)/(2.8e-50:315:82//Hs.155464:AF088219
 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519
 R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046
 5 R-HEMBA1005315//ESTs//1.9e-29:370:72//Hs.161483:N59169
 R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472
 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606
 R-HEMBA1005335//ESTs//1.7e-81:406:96//Hs.155374:AI341467
 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.
 10 129735:AF010144
 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350
 R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653
 R-HEMBA1005374//ESTs//1.5e-107:502:98//Hs.118208:AA947305
 R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150
 15 R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:
 92//Hs.43864:AA131568
 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278
 R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725
 R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059
 20 R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:
 45:99//Hs.4854:AF041248
 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391
 25 R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745981
 R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA204494
 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353
 R-HEMBA1005472//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:
 K00627
 30 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445
 R-HEMBA1005497
 R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788
 R-HEMBA1005506//75 kDa infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//
 Hs.62608:S58544
 35 R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870
 R-HEMBA1005511//ESTs, Weakly similar to similiar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:
 AI219740
 R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322
 R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045
 40 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981
 R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788
 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.
 17035:AI080471
 R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350
 45 R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926
 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627
 R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193
 R-HEMBA1005568//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.4e-31:
 182:76/Hs.133526:N21103
 50 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:A/280497
 R-HEMBA1005577
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392
 55 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539
 R-HEMBA1005588//Human c-yes 1 mRNA//2.6e-52:403:83//Hs.75680:M15990
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

R-HEMBA1005606//EST//1.0e-12:313.64//Hs.162402-AA573125
R-HEMBA1005609//ESTs//0.49:278.58//Hs.76235:W56390
R-HEMBA1005616//EST//1.3e-98:470.99//Hs.122230-AA781422
R-HEMBA1005621//ESTs,
5 Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539.92//Hs.
19400:AA662845
R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317.78//Hs.1721:X58377
R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279.65//Hs.15245.AF041081
R-HEMBA1005632//EST//1.5e-10:181.70//Hs.120259-AA731522
R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234.80//Hs.
10 10458:AF088219
R-HEMBA1005666//ESTs//2.3e-103:534.95//Hs.14512-AA205973
R-HEMBA1005670//ESTs//2.6e-39:166.81//Hs.139414:AI279477
R-HEMBA1005679//Esterase Diformylglutathione hydrolase//1.3e-50:322.88//Hs.82193:M13450
R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343.81//Hs.154103:AF061258
15 R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235.64//Hs.159437:
U44060
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//
1.7e-47:376.84//Hs.26988:U66406
R-HEMBA1005705//ESTs//3.0e-53:259.99//Hs.55314-AA772055
20 R-HEMBA1005717//EST//2.5e-59:287.99//Hs.146870:AI159943
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398.79//Hs.155481:
AJ006470
R-HEMBA1005737//ESTs//2.5e-57:416.83//Hs.23245-AA053815
R-nnnnnnnnnnnn//EST//0.098:125.68//Hs.136945:AA765672
25 R-HEMBA1005755//EST//2.2e-22:180.84//Hs.141488:N47096
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:
U21936
R-HEMBA1005780//ESTs//1.3e-106:512.97//Hs.11901-AA173974
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195.84//Hs.
30 10458:AF088219
R-HEMBA1005815//ESTs//7.6e-19:290.71//Hs.112218:AI038601
R-HEMBA1005822//ESTs//5.4e-49:246.98//Hs.34804-AA514980
R-HEMBA1005829//ESTs//2.7e-72:344.99//Hs.54548:AI039201
R-HEMBA1005834//ESTs//1.6e-44:317.82//Hs.157029:AI080618
35 R-HEMBA1005852//ESTs//1.6e-102:544.93//Hs.9911:AA098911
R-HEMBA1005853//ESTs//1.8e-78:398.95//Hs.140248:AA757917
R-HEMBA1005884//EST//2.6e-18:275.67//Hs.139357:AA420970
R-HEMBA1005891//ESTs//2.1e-89:427.98//Hs.67317:AI022252
R-HEMBA1005894
40 R-HEMBA1005909//ESTs//2.6e-91:436.99//Hs.147492:AI215686
R-HEMBA1005911//ESTs//1.1e-85:446.95//Hs.134494:AI076363
R-HEMBA1005921//ESTs//1.4e-84:428.95//Hs.127993:AA970632
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446.75//Hs.59403:
AB011098
45 R-HEMBA1005934//ESTs//0.20:142.65//Hs.97079:AA370867
R-HEMBA1005962//ESTs//1.8e-87:409.100//Hs.161292:AI199418
R-HEMBA1005963
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580.95//Hs.
26285:AF082516
50 R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551.70//Hs.148495:AF050199
R-HEMBA1005995//ESTs//7.5e-24:201.69//Hs.157029:AI080618
R-HEMBA1006002//ESTs//3.1e-112:573.95//Hs.61233:AI379875
R-HEMBA1006005//EST//1.0e-105:63//Hs.145273:AI249436
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444.67//Hs.26450:AB018268
55 R-HEMBA1006035//ESTs//4.5e-94:465.97//Hs.44625:N49951
R-HEMBA1006036//ESTs//6.1e-90:420.100//Hs.126771:AA916508
R-HEMBA1006042//EST//1.5e-88:424.98//Hs.132551:AA948490
R-nnnnnnnnnnnn

R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
 R-HEMBA1006090//ESTs//5.1e-66:320:99//Hs.99551:AA46171
 R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313
 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//
 5 Hs.73614:U83460
 R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293
 R-HEMBA1006124//ESTs//1.6e-20:286:64//Hs.148457:AI198931
 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
 10 R-nnnnnnnnnn/Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:
 AB007958
 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
 R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:RA41212
 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930
 15 R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627
 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H69606
 R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557
 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]/3.3e-114:581:95//
 20 Hs.23617:AA928683
 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:
 AF083384
 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881
 25 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]/1.2e-97:529:93//Hs.
 10552:AA524401
 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]/2.7e-88:484:
 92//Hs.104129:AA923278
 R-nnnnnnnnnn/H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
 30 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.
 cerevisiae]/1.6e-66:377:91//Hs.108674:W25621
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55298:AI084735
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037
 35 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:
 U33931
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]/5.6e-76:417:94//Hs.111754:
 AI204587
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)/2.8e-60:397:78//Hs.155464:AF088219
 40 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC
 REGION [Saccharomyces cerevisiae]/3.6e-119:582:97//Hs.42343:AI417075
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
 45 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
 R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:
 AB011166
 50 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5:82:84//Hs.23094:M19503
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2822:X64878
 55 R-HEMBA1006424//ESTs, Weakly similar to put ORF II [H.sapiens]/6.3e-13:263:66//Hs.43127:AA258004
 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05.487.58//Hs.32963:D31784
R-HEMBA1006461//ESTs//5.1e-78.393.97//Hs.142677:R95895
R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17.342.63//Hs.111730:AA604403
R-HEMBA1006471//ESTs//3.8e-66.370.92//Hs.14063:T77441
5 R-HEMBA1006474
R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40.365.78//Hs.
46468:U45984
R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92.517.91//Hs.132243:Y07701
R-HEMBA1006486//EST//7.0e-47.240.76//Hs.161917:AA483223
10 R-HEMBA1006489//ESTs//2.1e-93.440.99//Hs.125264:AA873350
R-HEMBA1006492//ESTs//0.00034:52.90//Hs.163219:AA810720
R-HEMBA1006494//EST//1.8e-06.192.67//Hs.141401:H93387
R-HEMBA1006497//ESTs//6.2e-45.232.97//Hs.118015:N33117
R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16.135.72//Hs.2161:M62505
15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117.570.96//Hs.153858:
AB014566
R-HEMBA1006521//ESTs//9.9e-99.496.96//Hs.64906:AA677300
R-HEMBA1006530//ESTs//0.18.260.60//Hs.24970:AI057628
R-HEMBA1006535//GS1 PROTEIN//0.52:267.62//Hs.78991:M86934
20 R-HEMBA1006540//EST//0.016:143.66//Hs.148189:AA897331
R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48.287.91//Hs.79507:AB011154
R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-
109:547.96//Hs.21122:A191594
R-HEMBA1006562//EST//1.1e-13.327.63//Hs.149641:AI283064
25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
R-HEMBA1006569//ESTs//4.7e-89.458.96//Hs.42861:W74725
R-HEMBA1006579//ESTs//2.9e-19.110:99//Hs.126191:AA873876
R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29.276.76//Hs.144563:
AF057280
30 R-HEMBA1006595//ESTs//1.3e-96.487.96//Hs.43228:N67390
R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219
R-HEMBA1006612
R-nnnnnnnnnnnn//ESTs//1.2e-25.225.80//Hs.138852:AA284247
R-HEMBA1006624//ESTs//1.9e-93.454.98//Hs.72531:AA773630
35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60.286.90//Hs.22271:D26067
R-HEMBA1006635//ESTs, Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]//2.7e-
91:426:100//Hs.139469:AI299889
R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:
100//Hs.109818:AA411185
40 R-HEMBA1006643//ESTs//1.8e-35:189.97//Hs.139640:AA846777
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:
U40282
R-HEMBA1006652//ESTs//7.6e-100.536.93//Hs.142613:AA129427
R-HEMBA1006653//ESTs//2.0e-33:181.87//Hs.153598:AI282511
45 R-HEMBA1006665//EST//1.2e-13:141.72//Hs.145596:AI263102
R-HEMBA1006674//ESTs//3.1e-32:212.83//Hs.95115:AA206594
R-HEMBA1006676//ESTs//2.6e-95.5:10.93//Hs.39140:AI041842
R-HEMBA1006682//EST//1.4e-05:277.62//Hs.145762:AI269435
R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:
50 261:79//Hs.77579:AF013263
R-HEMBA1006696//ESTs//4.5e-95.448.99//Hs.155694:AI032695
R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92.483.94//Hs.
6525:AI205313
R-HEMBA1006709//ESTs//3.4e-25.207.80//Hs.88617:AA872062
55 R-HEMBA1006717
R-HEMBA1006737//EST//5.9e-30.317.75//Hs.140568:AA826002
R-HEMBA1006744//Interleukin 10//3.7e-41:419.74//Hs.2180:M57627
R-HEMBA1006754//ESTs//1.2e-46.276.83//Hs.141254:AI334099

R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
 5 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978
 R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
 10 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
 R-nnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:
 15 AB018315
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
 R-HEMBA1006921//ESTs//3.2e-33:170:100//Hs.152277:AA593117
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400
 20 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:
 AJ010841
 25 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
 30 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363
 R-HEMBA1007045
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
 R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
 R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-
 40 40:163:83//Hs.152369:AA504818
 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
 R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
 R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272
 45 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
 R-HEMBA1007147
 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
 R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
 R-nnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085
 50 R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954
 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987
 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:
 55 AB018340
 R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
 R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
 R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207
 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
 R-HEMBA1007286//EST//9.4e-43:344:81//Hs.162112:AA524804
 5 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
 R-HEMBA1007301
 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
 R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:
 AA205569
 10 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:
 K00629
 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.
 154069:U06452
 R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
 15 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
 R-HEMBB1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403
 R-HEMBB1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-
 20 40:292:83//Hs.129708:AF064090
 R-HEMBB1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
 R-HEMBB1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
 R-HEMBB1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
 R-HEMBB1000030//ESTs//3.2e-76:373:97//Hs.140190:TA01449
 R-HEMBB1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME
 25 III [Caeorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA18465
 R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//
 Hs.20815:AF084928
 R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
 R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954
 30 R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:AI357802
 R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903
 R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107
 R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-
 35 UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584
 R-HEMBB1000059//ESTs//1.7e-20:200:70//Hs.163954:N75939
 R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
 R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353
 R-HEMBB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
 R-HEMBB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:
 40 AB014540
 R-HEMBB1000113//EST//2.2e-94:437:100//Hs.136893:AA805239
 R-HEMBB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
 R-HEMBB1000136//ESTs//0.043:262:59//Hs.61304:AA025692
 R-HEMBB1000141//ESTs//5.0e-05:254:79//Hs.141652:N77915
 45 R-HEMBB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
 R-HEMBB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
 R-HEMBB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
 R-HEMBB1000198//ESTs//1.0123:62//Hs.116602:AA665965
 R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353
 50 R-HEMBB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364
 R-HEMBB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-
 48:292:79//Hs.133089:AF064019
 R-HEMBB10002267//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME
 II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214
 55 R-HEMBB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106
 R-HEMBB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219
 R-HEMBB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783
 R-HEMBB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

R-HEMBB1000264
R-HEMBB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]/2.7e-102:556:93//
Hs.16079:AA083522
R-HEMBB1000272//ESTs/4.3e-91:480:94//Hs.107467:H11385
5 R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:
AB011129
R-HEMBB1000284//ESTs/4.8e-64:389:91//Hs.118043:N50458
R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353
R-HEMBB1000312//ESTs/6.0e-23:272:73//Hs.121354:AA758601
10 R-HEMBB1000317//ESTs/7.3e-90:424:99//Hs.150042:AI298034
R-HEMBB1000318//Smal inducible cytokine A5 (RANTES)/3.3e-41:318:80//Hs.155464:AF088219
R-HEMBB1000335//ESTs/3.7e-15:324:65//Hs.85077:AA968576
R-HEMBB1000336//ESTs/6.4e-76:402:95//Hs.17207:H92480
R-HEMBB-1000337//ESTs/2.1e-80:391:97//Hs.118990:AI378084
15 R-HEMBB1000338//Smal inducible cytokine A5 (RANTES)/4.0e-39:274:85//Hs.155464:AF088219
R-HEMBB1000339//EST/5.8e-41:336:79//Hs.151873:AA205736
R-HEMBB1000341//ESTs/3.8e-19:310:68//Hs.37573:H59651
R-HEMBB1000343//EST/1.1e-77:396:95//Hs.162664:AA605020
R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008
20 R-HEMBB1000369//ESTs//1.6e-21:234:73//Hs.1151583:AA463590
R-HEMBB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.
92381:AB007956
R-HEMBB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969
R-HEMBB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840
25 R-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642
R-HEMBB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173
R-HEMBB1000404//ESTs//0.088:298:59//Hs.61607:AA032026
R-HEMBB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591
R-HEMBB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087
30 R-HEMBB1000438//ESTs, Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//0.30:214:63//
Hs.142209:AA873303
R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990
R-HEMBB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221
R-HEMBB1000455//EST/4.8e-14:42:65//Hs.68832:AA088438
35 R-HEMBB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396
R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390
R-HEMBB1000487//EST//0.78:87:68//Hs.134601:AI081506
R-HEMBB1000490//Small inducible cytokine A5 (RANTES)/4.0e-39:320:80//Hs.155464:AF088219
R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080
40 R-HEMBB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125
R-HEMBB1000510//EST//1.4e-45:139:97//Hs.152260:AA488703
R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
R-HEMBB1000530//ESTs//2.7e-73:425:90//Hs.141254:A134099
45 R-HEMBB1000550//EST//2.9e-11:113:79//Hs.161503:N68662
R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:
AF052288
R-HEMBB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986
R-HEMBB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258
50 R-HEMBB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709
R-HEMBB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618
R-HEMBB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
R-HEMBB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
R-HEMBB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
55 R-HEMBB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
R-HEMBB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
R-HEMBB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125
R-HEMBB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

R-HEMBB1000631//ESTs//5.1e-100:508.96//Hs.110379:N58152
 R-HEMBB1000632//ESTs//6.2e-44:371.80//Hs.132722:AA618531
 R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254.86//Hs.74554:D38522
 R-HEMBB1000638//EST//2.2e-38:371.76//Hs.162236:AA55182
 5 R-HEMBB1000643//ESTs//0.0049:191.62//Hs.W51963
 R-HEMBB1000649//ESTs, Moderately similar to hTAFI68 [H.sapiens]//4.0e-76:399.95//Hs.124106:AA948100
 R-HEMBB1000652//ESTs//1.5e-14:271.64//Hs.163954:N57939
 R-HEMBB1000665//ESTs//4.2e-12:109.87//Hs.41407:W94988
 R-HEMBB1000671//ESTs//2.8e-68:439.87//Hs.140491:W52705
 10 R-HEMBB1000673//EST//0.58:46.82//Hs.142286:AA338293
 R-HEMBB1000684//ESTs//8.5e-20:307.72//Hs.122825:AA765454
 R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287.93//Hs.158300:AF040723
 R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165.78//Hs.155464:AF088219
 R-HEMBB1000706//EST//1.2e-10:211.65//Hs.105524:AA521412
 15 R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245.99//Hs.111730:AA604403
 R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350.59//Hs.10351:AB002306
 R-HEMBB1000726//EST//5.3e-49:303.88//Hs.149580:AI281881
 R-HEMBB1000738//Homo sapiens mRNA, clone:RE54-16//2.5e-49:302.89//Hs.121493:D25272
 R-HEMBB1000749//ESTs//1.6e-49:331.86//Hs.152788:AA630925
 20 R-HEMBB1000763//ESTs//9.7e-104:474.95//Hs.77480:AA100522
 R-HEMBB1000770//EST//1.0e-75:359.99//Hs.138564:AA642445
 R-HEMBB1000781//ESTs//5.3e-66:317.99//Hs.28827:AI125541
 R-HEMBB1000789//ESTs//5.9e-83:394.99//Hs.120842:AA435771
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193.75//Hs.73734:Z23091
 25 R-HEMBB1000794//ESTs//7.1e-98:490.96//Hs.105743:AA532718
 R-HEMBB1000807//ESTs//2.6e-22:145.02//Hs.53913:AA908961
 R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206.79//Hs.155464:AF088219
 R-HEMBB1000821//ESTs//2.4e-90:425.99//Hs.118659:AI052447
 R-HEMBB1000822//ESTs//1.7e-45:288.89//Hs.24130:R27124
 30 R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245.82//Hs.155464:AF088219
 R-HEMBB1000827//EST//2.8e-40:295.84//Hs.149580:AI281881
 R-HEMBB1000831//ESTs//4.0e-59:291.98//Hs.62675:AA044176
 R-HEMBB1000835//ESTs//7.3e-21:124.82//Hs.102671:N52545
 R-HEMBB1000840//ATPase, Na⁺/K⁺ transporting, beta 2 polypeptide//1.3e-43:163.84//Hs.78854:AF007876
 35 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367.78//Hs.129740:AB011137
 R-HEMBB1000852//EST//1.2e-09:188.70//Hs.127869:AA968599
 R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)/1.0e-41:483.73//Hs.2379:U23942
 R-HEMBB1000876//EST//0.0022:21.63//Hs.125552:AA884141
 40 R-HEMBB1000883//ESTs//1.4e-65:343.95//Hs.98269:H27247
 R-HEMBB1000887//ESTs//4.0e-22:212.79//Hs.138965:AI004740
 R-HEMBB1000888//EST//8.2e-07:196.64//Hs.118276:W15258
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327.83//Hs.51048:X68830
 R-HEMBB1000893//EST//4.7e-24:242.85//Hs.149580:AI281881
 45 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
 R-HEMBB1000910//ESTs//1.9e-36:318.78//Hs.141140:AA715983
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367.73//Hs.149323:AB002325
 R-HEMBB1000915//ESTs//0.0018:188.61//Hs.44847:AI222742
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228.84//Hs.127649:AB007874
 50 R-HEMBB1000927//ESTs//2.2e-62:307.98//Hs.97044:AA365784
 R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350.91//Hs.49163:AA532881
 R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546.86//Hs.23094:MI9503
 R-HEMBB1000973//ESTs//6.8e-95:445.99//Hs.105859:AI419354
 R-HEMBB1000975//ESTs//1.2e-39:197.100//Hs.26176:AI032007
 55 R-HEMBB1000981//EST//7.7e-58:284.98//Hs.60179:AA007242
 R-HEMBB1000985//ESTs//1.2e-103:524.95//Hs.43102:AA131369
 R-HEMBB1000991//EST//0.99:58.72//Hs.100246:T23625
 R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482.70//Hs.154103:AF061258

R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
 R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:
 H58762
 R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
 5 R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
 R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080
 R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
 R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
 R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
 10 R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107
 R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:
 AB014518
 R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:
 AB007944
 15 R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
 R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
 R-HEMBB1001068//Homo sapiens liprin-beta 2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803
 R-HEMBB1001096//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233:70//Hs.37181:D64108
 R-HEMBB1001102//Human mRNA for KIAA0356 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353
 20 R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080
 R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
 R-HEMBB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092
 R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
 R-HEMBB1001126
 25 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:
 285:73//Hs.554:M25077
 R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962
 R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881
 R-HEMBB1001151
 30 R-HEMBB1001153//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.3e-
 65:331:96//Hs.154179:AA579197
 R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878
 R-nnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162
 R-HEMBB1001177
 35 R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349
 R-HEMBB1001199
 R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183
 R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549
 R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573
 40 R-HEMBB1001218//Kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,
 antigen detected by monoclonal and antibody I4))//3.1e-44:298:87//Hs.103458:X53795
 R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817
 R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//
 Hs.71873:AA148213
 45 R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560
 R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236
 R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987
 R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268
 R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.
 50 159897:AB007970
 R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087
 R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412
 R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III
 [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021
 55 R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840
 R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112
 R-HEMBB1001302
 R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

- R-HEMBB1001314//Interleukin 10/6.3e-41:334:79//Hs.2180;M57627
 R-HEMBB1001315//Interleukin 10/1.9e-43:285:87//Hs.2180;M57627
 R-HEMBB1001317//Human cytochrome P450-1IB (h11B3) mRNA, complete cds//8.4e-45:357:81//Hs.110194: M29873
 5 R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754
 R-HEMBB1001331//ESTs, Weakly similar to DFS7 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222
 R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365
 R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639
 R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470
 10 R-HEMBB1001346
 R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354
 R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721
 R-HEMBB1001364//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055
 15 R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087
 R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R96917
 R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219
 R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
 R-HEMBB1001384//ESTs//6.6e-110:547:98//Hs.6671:AI341699
 20 R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
 R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
 R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342
 R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
 R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
 25 R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846
 R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
 R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
 R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
 R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
 30 R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
 R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
 R-HEMBB1001464//ESTs, Weakly similar to KO1H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468
 R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481
 R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515
 35 R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630: AB018280
 R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
 R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
 40 R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
 R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
 R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869
 R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274
 R-HEMBB1001562//EST//4.7e-43:316:83//Hs.151365:AA63962
 45 R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521
 R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
 R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
 R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
 R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015
 50 R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184
 R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
 R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888
 R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-5//5.7e-41:193:90//Hs.121493:D25272
 R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082
 55 R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
 R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813
 R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA086438
 R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572
 R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573.97//Hs.24439:
 AB014546
 R-HEMBB1001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534
 5 R-HEMBB1001685//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-
 43:292:86//Hs.96337:AA225358
 R-HEMBB1001695//ESTs//3.7e-101:539.94//Hs.78289:R60867
 R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038
 R-HEMBB1001706//ESTs//1.3e-39:308.81//Hs.141318:N71080
 10 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:
 AA205569
 R-HEMBB1001711//ESTs//1.6e-34:225:87//Hs.57883:AA218645
 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
 8.6e-11:158.71//Hs.141263:H64113
 15 R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403
 R-HEMBB1001747//EST//9.9e-55:293.81//Hs.112866:AA620488
 R-HEMBB1001749//ESTs//2.5e-13:95.91//Hs.139888:N25287
 R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059
 R-HEMBB1001756//EST//2.6e-06:165.64//Hs.121195:AA757211
 20 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264.74//Hs.70008:
 L00352
 R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152768:AA211369
 R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406
 R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253
 25 R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391
 R-HEMBB1001812//ESTs//1.2e-21:91:78//Hs.138852:AA284247
 R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503
 R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-
 106:498:98//Hs.159396:AF056209
 30 R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.
 67619:AB007957
 R-HEMBB1001839
 R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125
 R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539
 35 R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106
 R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397
 R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434
 R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA487980
 R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572
 40 R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240
 R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081
 R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310
 R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191
 R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725
 45 R-HEMBB1001908//Homo sapiens EV15 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915
 R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216
 R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750
 R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897
 R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390
 50 R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:
 70//Hs.153086:Y11251
 R-HEMBB1001925//Human mRNA for KIAA0392 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325
 R-HEMBB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875
 R-HEMBB1001944//EST//0.034:228:57//Hs.93664:N23366
 55 R-HEMBB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875
 R-HEMBB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589
 R-HEMBB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998
 R-HEMBB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

R-HEMBB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284.83//Hs.74554:D38522
 R-HEMBB1001957//EST/4.8e-50:382.81//Hs.149580:AI281881
 R-HEMBB1001962//ESTs/1.5e-20:143.88//Hs.11924:W26972
 R-HEMBB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296.88//Hs.153468:
 5 AB011147
 R-HEMBB1001973//ESTs/1.4e-48:303.88//Hs.132722:AA618531
 R-HEMBB1001983//ESTs/2.6e-72:374.95//Hs.141022:H06475
 R-HEMBB1001988//ESTs/2.0e-31:204.88//Hs.142531:N91572
 R-HEMBB1001990//ESTs/9.4e-115.574.96//Hs.44426:AA173223
 10 R-HEMBB1001996
 R-HEMBB1001997//ESTs//7.6e-78:380.98//Hs.32682:H37798
 R-HEMBB1002002//Human kpnI repeat mma (cdna clone pcd-kpnI-8), 3' end//3.0e-18:222.71//Hs.103948:
 K00627
 R-HEMBB1002005//EST//2.2e-41:339.80//Hs.160833:AI345334
 15 R-HEMBB1002009//EST/2.9e-44:245.94//Hs.28788:R66996
 R-HEMBB1002015//EST/0.0027:198.63//Hs.160868:AI359052
 R-HEMBB1002042//ESTs/1.1e-75:529.84//Hs.106919:AA523900
 R-HEMBB1002043//ESTs//7.9e-40:292.83//Hs.70279:AA757426
 R-HEMBB1002044//ESTs/2.1e-92:460.94//Hs.115897:AA1566638
 20 R-HEMBB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301.85//Hs.113283:AF018080
 R-HEMBB1002049//ESTs//3.8e-77:409.94//Hs.122624:R82638
 R-HEMBB1002050//ESTs/8.7e-45:330.82//Hs.44702:AI148840
 R-HEMBB1002068//ESTs//8.3e-70:333.99//Hs.134807:AI090671
 R-HEMBB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486.81//Hs.
 25 129735:AF010144
 R-HEMBB1002092//ESTs/6.5e-46:331.83//Hs.22910:W18193
 R-HEMBB1002094//EST//3.6e-45:280.88//Hs.149580:AI281881
 R-HEMBB1002115
 R-HEMBB1002139//ESTs/4.2e-45:318.85//Hs.107657:AA126814
 30 R-HEMBB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//
 1.4e-45:281.88//Hs.125231:AF068006
 R-HEMBB1002152//EST/4.3e-39:250.89//Hs.156552:AA833553
 R-HEMBB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328.85//Hs.96247:X95073
 R-HEMBB1002190//ESTs//8.3e-05:122.70//Hs.41974:AF039185
 35 R-HEMBB1002193//Human sky mRNA for Skty, complete cds//8.9e-24:398.69//Hs.301:U18934
 R-HEMBB1002217//EST//6.6e-50:303.89//Hs.149580:AI281881
 R-HEMBB1002218//ESTs//2.3e-19:150.86//Hs.136031:W95841
 R-HEMBB1002232//ESTs//8.9e-47:445.77//Hs.163971:N72584
 R-HEMBB1002247//EST//6.6e-09:236.65//Hs.130578:AI004631
 40 R-HEMBB1002249//ESTs/5.2e-16:325.64//Hs.156253:AI334807
 R-HEMBB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590.88//Hs.23094:M19503
 R-HEMBB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342.83//Hs.84123:AB002363
 R-HEMBB1002266//ESTs//4.4e-98:472.98//Hs.65366:AI189112
 R-HEMBB1002280//EST//2.8e-14:247.90//Hs.161917:AA482323
 45 R-HEMBB1002300//ESTs//8.4e-19:229.75//Hs.138463:N72305
 R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138.67//Hs.155174:AB007892
 R-HEMBB1002327//EST//0.042:249.61//Hs.121097:AA714637
 R-HEMBB1002329//ESTs//1.7e-94:453.99//Hs.7114:R24312
 R-HEMBB1002340//ESTs//5.8e-15:163.77//Hs.26378:H10228
 50 R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46.84//Hs.42644:AJ010841
 R-HEMBB1002358//ESTs//2.0e-52:319.81//Hs.140255:AA708322
 R-HEMBB1002359//ESTs//2.7e-106:517.97//Hs.13634:AI051613
 R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360.65//Hs.74554:D38522
 R-HEMBB1002371//Catalase//3.3e-22:235.77//Hs.76359:X04085
 55 R-HEMBB1002381//Homo sapiens (JHB) mRNA, partial cds//1.0e-08:120.78//Hs.142296:AF072467
 R-HEMBB1002383//ESTs//3.5e-108:520.98//Hs.45140:D90055
 R-HEMBB1002387
 R-HEMBB1002415//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//2.3e-23:

168.77//Hs.133526.N21103
R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304.90//Hs.144563:
AF057280
R-HEMBB1002424//ESTs//2.7e-48:289.87//Hs.155243.N70293
5 R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292.87//Hs.153014:AB002353
R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546.71//Hs.154326:D42087
R-HEMBB1002458//EST//1.8e-72:343.100//Hs.162006:AA508089
R-HEMBB1002477//ESTs//1.6e-38:215.93//Hs.18240:AA460083
R-HEMBB1002489//ESTs//1.2e-101:534.94//Hs.7981:H15176
10 R-HEMBB1002492//ESTs//5.0e-14:350.62//Hs.99205:AA204969
R-HEMBB1002495//ESTs//2.1e-19:147.86//Hs.163747:AA174017
R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336.98//Hs.141515:T41142
R-HEMBB1002509//ESTs//2.7e-97:459.99//Hs.127638:AI014615
R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265.95//Hs.48827:AA873278
15 R-HEMBB1002520//EST//7.2e-40:198.84//Hs.140493:AA804538
R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142.69//Hs.
159301:U43672
R-HEMBB1002531//EST//0.024:147.61//Hs.148305:AA909605
R-HEMBB1002534//EST//3.1e-22:168.84//Hs.146794:AI149478
20 R-HEMBB1002545//ESTs//9.2e-90:421.99//Hs.118317:AI033259
R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210.81//Hs.11896:
T68813
R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344.82//Hs.51048:X68830
R-HEMBB1002579//ESTs//4.6e-47:326.85//Hs.155184:AA573189
25 R-HEMBB1002582//ESTs//0.00036:91.76//Hs.140039:AA047045
R-HEMBB1002590//ESTs//1.0e-37:210.84//Hs.36658:N91138
R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297.87//Hs.154326:D42087
R-HEMBB1002600//EST//2.5e-17:147.84//Hs.121918:AA777424
R-HEMBB1002601//ESTs//7.8e-68:358.95//Hs.101489:R66923
30 R-HEMBB1002603//EST//1.1e-47:281.90//Hs.149580:AI281881
R-HEMBB1002607//ESTs//5.4e-75:379.97//Hs.29438:H42896
R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:
140.70//Hs.155456:AA707265
R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278.83//Hs.
35 159187:AB007977
R-HEMBB1002614//ESTs//3.4e-81:383.99//Hs.13012:AI094150
R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151.80//Hs.
137574:AF055917
R-HEMBB1002623//ESTs//1.6e-45:288.87//Hs.138852:AA284247
40 R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278.81//Hs.155464:AF088219
R-HEMBB1002664//EST//8.9e-49:315.87//Hs.149580:AI281881
R-HEMBB1002677//ESTs//0.65:159.62//Hs.163517:AI419775
R-HEMBB1002683//H.sapiens mRNA for delta 4-3oxosteroid 5 beta-reductase//8.6e-54:543.75//Hs.2638:
Z28339
45 R-HEMBB1002684//ESTs//3.0e-18:148.87//Hs.158270:AA776646
R-HEMBB1002686//ESTs//6.1e-80:419.96//Hs.103002:W02753
R-HEMBB1002692//ESTs//3.3e-58:451.82//Hs.141254:AI34099
R-HEMBB1002697//ESTs//6.2e-86:423.98//Hs.129812:AA769487
R-HEMBB1002699//EST//5.6e-46:322.84//Hs.140231:AI054398
50 R-HEMBB1002702//ESTs//5.6e-36:412.72//Hs.154993:AA142842
R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN I//0.024:412.58//Hs.74648:M73547
R-HEMBB1002712//ESTs//9.0e-96:451.99//Hs.136806:AA805682
R-MAMMA100009//ESTs//3.0e-78:392.96//Hs.163947:AA678701
R-MAMMA100019//Small inducible cytokine A5 (RANTES)//1.5e-47:247.87//Hs.155464:AF088219
55 R-MAMMA100020//Zinc finger protein 2 (A-5)/4.9e-49:384.80//Hs.155533:X60152
R-MAMMA100025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154.71//Hs.32511:AB007901
R-MAMMA100043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277.84//Hs.93121:
AB018304

R-MAMMA100045//ESTs//1.0e-38:225:92//Hs.142567:AA287165
 R-MAMMA100055//ESTs//10.14:91:67//Hs.144061:AA996350
 R-MAMMA100057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)///3.8e-77:545:83//Hs.69747:M5531
 5 R-MAMMA100069//ESTs//8.0e-108:546:96//Hs.44856:N37065
 R-MAMMA100084//Homo sapiens clone 23632 mRNA sequence///7.3e-43:313:83//Hs.46918:AF052099
 R-MAMMA100085//ESTs, Highly similar to PUTATIVE CYSTEINYLN-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241
 R-MAMMA100092//EST, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//4.2e-
 10 22:287:71//Hs.136063:U51713
 R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:
 L00352
 R-MAMMA1000117//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.1e-08:
 96:80//Hs.115088:AA230172
 15 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577
 R-MAMMA1000133
 R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017
 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.
 159867:AB007970
 20 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881
 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:
 562:75//Hs.77579:AF013263
 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787
 R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:
 25 AJ224162
 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:
 90//Hs.90367:AI357069
 R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611
 R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054
 30 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881
 R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:
 AA421103
 R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425
 R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946
 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:
 AB018315
 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-
 43:315:83//Hs.129708:AF064090
 R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
 40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238
 R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
 R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.
 159187:AB007977
 R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369
 45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
 R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.
 92381:AB007956
 R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
 R-MAMMA1000287
 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892
 R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067
 R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251
 R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434
 R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
 55 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:
 AA662998
 R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159
 R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912
 5 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087
 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659
 R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
 R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
 R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:
 92//Hs.32170:AB015132
 10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060
 R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]
 //9.1e-47:316:81//Hs.138698:N38973
 R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198
 R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:
 15 AB007958
 R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
 R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:
 282:82//Hs.97203:UB3171
 R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
 20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
 R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
 R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.
 154069:U06452
 R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
 25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:
 302:85//Hs.97203:UB3171
 R-MAMMA1000444//Cytokine modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
 R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
 R-MAMMA1000458
 30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
 R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
 R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
 R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886
 R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
 35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)/4.7e-43:283:86//Hs.155464:AF088219
 R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
 R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
 R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
 40 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
 R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
 R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
 R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872
 R-MAMMA1000585//ESTs//5.1e-33:78//Hs.130315:AA936548
 45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)/3.0e-45:225:80//Hs.155464:AF088219
 R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
 R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.
 116007:S79267
 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN
 50 SIS1-MRP12 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105
 R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
 R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
 R-MAMMA1000623
 R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
 55 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
 R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:
 AJ224162
 R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

- R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]/I.8.4e-98:464.98//Hs.31431:AI022065
- R-MAMMA1000672//ESTs/2.0e-80:382.99//Hs.106747:AI080476
- R-MAMMA1000684//ESTs/6.2e-72:357.98//Hs.67896:AA65212
- 5 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216.75//Hs.98938:AB002343
- R-MAMMA1000707//EST//7.0e-11:195.68//Hs.147002:AI184644
- R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485.74//Hs.153563:AF011333
- R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158.79//Hs.142764:AA205569
- 10 R-MAMMA1000718//ESTs/3.1e-45:264.88//Hs.152413:AA780515
- R-MAMMA1000720//ESTs/7.4e-44:244.87//Hs.111742:R39329
- R-MAMMA1000723//Homo sapiens mRNA for alpha(I,2)fucosyltransferase, complete cds//5.6e-52:350.82//Hs.46328:D87942
- R-MAMMA1000731//ESTs//1.1e-19:420.66//Hs.35036:H95267
- 15 R-MAMMA1000732//EST//2.9e-20:229.74//Hs.135400:AI056893
- R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371.74//Hs.141429:AA631915
- R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253.98//Hs.31575:AF100141
- R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya bisexualis antheridial steroid receptor [C.elegans]//2.3e-116:557.98//Hs.71472:AA632288
- 20 R-MAMMA1000744//ESTs/0.015:143.67//Hs.135382:AI224205
- R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568.86//Hs.23094:M19503
- R-MAMMA1000752//Interleukin 10//2.8e-43:339.80//Hs.2180:M57627
- R-MAMMA1000760//EST//5.0e-44:306.86//Hs.162404:AA573131
- 25 R-MAMMA1000761//EST//5.0e-41:187.85//Hs.162335:AA564256
- R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465.76//Hs.153014:AB002353
- R-MAMMA1000776//ESTs//1.9e-43:429.73//Hs.141742:W22204
- R-MAMMA1000778//ESTs/1.8e-31:445.70//Hs.111723:H57439
- R-MAMMA1000782//EST//0.0019:102.68//Hs.120686:AA747150
- 30 R-MAMMA1000798//ESTs//1.4e-13:267.69//Hs.140156:AA704163
- R-MAMMA1000802//Clathrin, light polypeptide (Lcb) //1.5e-45:358.76//Hs.73919:X81637
- R-MAMMA1000831//ESTs/1.3e-1.04:510.97//Hs.17494:AA572675
- R-MAMMA1000839//EST//2.9e-51:307.89//Hs.149580:AI281881
- R-MAMMA1000841//ESTs/1.3e-34:412.72//Hs.121256:AA757902
- 35 R-MAMMA1000842//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//9.4e-44:363.79//Hs.96337:AA225358
- R-MAMMA1000843//ESTs/2.2e-106:525.97//Hs.152016:AA603097
- R-MAMMA1000845//ESTs/1.6e-66:327.98//Hs.156900:AA468955
- R-MAMMA1000851//ESTs/3.7e-14:115.86//Hs.140590:R76251
- 40 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281.91//Hs.40100:AB002390
- R-MAMMA1000856//EST//1.8e-16:150.79//Hs.136811:AA789212
- R-MAMMA1000862//EST//3.2e-05:93.73//Hs.161205:AI419311
- R-MAMMA1000863//ESTs//1.0e-46:446.73//Hs.153432:AA098922
- R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324.80//Hs.46918:AF052099
- 45 R-MAMMA1000867//ESTs/9.8e-16:193.76//Hs.152340:AA521399
- R-MAMMA1000875//EST//3.1e-24:301.72//Hs.132635:AI032875
- R-MAMMA1000876//ESTs/9.9e-48:246.97//Hs.112165:AA621243
- R-MAMMA1000878//ESTs//1.4e-38:324.79//Hs.141024:H07128
- R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542.68//Hs.154872:
- 50 AB011166
- R-MAMMA1000883//ESTs//1.0:207.60//Hs.47199:N51107
- R-MAMMA1000897//ESTs/2.6e-78:383.97//Hs.41067:AI310215
- R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307.91//Hs.146395:AB002329
- R-MAMMA1000906//ESTs/8.0e-25:206.83//Hs.141825:AA017093
- 55 R-MAMMA1000908//ESTs/4.4e-32:176.96//Hs.38559:AA701634
- R-MAMMA1000914//ESTs//0.032:150.63//Hs.119162:AA399989
- R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PiPK) mRNA, complete cds//7.7e-38:269.74//Hs.108966:U48696

R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335
 R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727
 R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281
 R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428
 5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:
 80//Hs.1381:MM5053
 R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178
 R-MAMMA1000957//Kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody I4A))//7.5e-49:340:85//Hs.103458:X53795
 10 R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:
 AB011147
 R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
 R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
 R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:
 15 AB018304
 R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
 R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:
 445.77//Hs.77579:AF013263
 R-MAMMA1001003//Sialophorin (gp115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075
 20 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313
 R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333
 R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
 R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
 R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461
 25 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390
 R-nnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122825:R68650
 R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881
 R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:
 AI015487
 30 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
 R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
 R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
 R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
 R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
 35 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
 R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
 R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
 6.4e-34:262:82//Hs.129727:AF035587
 R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.
 40 61840:U28866
 R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576
 R-MAMMA1001126//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.
 116007:S79267
 R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750
 45 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
 R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
 R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179
 R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
 R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750
 50 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970
 R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
 R-MAMMA1001188//ESTs//3.8e-85:410:99//Hs.163811:W44959
 R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
 R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.
 55 musculus]//2.6e-80:358:96//Hs.163827:AA074202
 R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
 R-MAMMA1001203//Clathrin, light polypeptide (Lcb) //2.8e-65:348:79//Hs.73919:X81637
 R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

R-MAMMA1001215//ESTs//1.3e-43:158.86//Hs.155243:N70293
 R-MAMMA1001220//ESTs//8.9e-17:276.68//Hs.116518:AA653202
 R-MAMMA1001222//ESTs//0.49:112.66//Hs.24668:AA897315
 R-MAMMA1001243//EST//0.99:143.62//Hs.68522:C20701
 5 R-MAMMA1001244//ESTs//2.2e-06:79.83//Hs.123163:AA805619
 R-MAMMA1001249//ESTs//4.2e-68:343.97//Hs.147139:AI191307
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221.77//Hs.142764:
 AA205569
 R-MAMMA1001259//ESTs//1.3e-43:266.90//Hs.6193:AA045149
 10 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226.75//Hs.65238:
 AB014561
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181.85//Hs.146333:X81001
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus mus-
 15 culus]//1.1e-108:546.95//Hs.18999:N30643
 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188.94//Hs.14409:
 AB011144
 R-MAMMA1001280//EST//0.0015:170.62//Hs.116770:AA630371
 R-MAMMA1001292//ESTs//5.6e-102:481.99//Hs.94810:AA811876
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348.70//Hs.15731:
 20 AB011135
 R-MAMMA1001298//ESTs//1.4e-44:375.79//Hs.70279:AA757426
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300.85//Hs.
 46468:L45984
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188.70//Hs.
 25 55771:AF004709
 R-MAMMA1001324//ESTs//5.3e-68:297.88//Hs.121228:AA709471
 R-MAMMA1001330//ESTs//1.6e-57:429.83//Hs.70279:AA757426
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285.75//Hs.32567:AF073519
 R-MAMMA1001343//ESTs//8.1e-51:273.93//Hs.162208:AA536127
 30 R-MAMMA1001346//ESTs//1.0:122.65//Hs.33028:AA482478
 R-MAMMA1001383//ESTs//1.4e-45:377.80//Hs.114671:N39322
 R-MAMMA1001388//EST//7.7e-47:361.80//Hs.162197:AA535216
 R-MAMMA1001397//EST//8.7e-48:337.83//Hs.149598:AI281881
 R-MAMMA1001408//EST//1.2e-38:251.87//Hs.162677:AA604831
 35 R-MAMMA1001411//ESTs//4.3e-93:435.99//Hs.105460:AA780275
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117.96//Hs.
 19122:AF038957
 R-MAMMA1001420//ESTs//7.3e-96:507.95//Hs.55299:AI335267
 R-MAMMA1001435//ESTs//5.0e-97:459.99//Hs.144843:AI222168
 40 R-MAMMA1001442//ESTs//7.1e-28:167.83//Hs.141019:AA287618
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328.67//Hs.155174:AB007892
 R-MAMMA1001452//EST//5.6e-44:487.75//Hs.161476:N57542
 R-MAMMA1001465
 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:
 45 66//Hs.136529:AF058317
 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328.78//Hs.43681:AL022394
 R-MAMMA1001501//ESTs//4.6e-100:472.98//Hs.123660:AA813065
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220.69//Hs.74554:D38522
 R-MAMMA1001510
 50 R-MAMMA1001522//ESTs//3.2e-16:214.75//Hs.152816:AA634242
 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282.89//Hs.66710:X96969
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA,
 complete cds//1.9e-56:489.76//Hs.108966:U48696
 R-MAMMA1001575//ESTs//4.3e-92:440.98//Hs.162882:AA807140
 55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549.96//Hs.
 21635:AI417305
 R-MAMMA1001590//ESTs//1.1e-63:324.96//Hs.142217:AA278441
 R-MAMMA1001600//ESTs//5.6e-15:159.78//Hs.138633:H98792

R-MAMMA1001604
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488.96//Hs.143263:
AI057616
R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408.76//Hs.121493:D25272
5 R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472.76//Hs.15519:
AB018315
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168.73//Hs.115216-AA291074
R-MAMMA1001633//EST//5.1e-14:228.68//Hs.141456:N36377
R-MAMMA1001635//ESTs//3.4e-37:368.75//Hs.164033:AA769606
10 R-MAMMA1001649
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272.81//
Hs.129735:AF010144
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304.89//Hs.155464:AF088219
R-MAMMA1001671//EST//1.9e-14:312.65//Hs.137153:R46248
15 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation inhibitor 1//0.066:196.62//Hs.159161:X69550
R-MAMMA1001683//ESTs//4.9e-94:447.98//Hs.134464:AI151081
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246.73//Hs.
67619:AB007957
R-MAMMA1001692//Human mRNA for KIAA0063 gene, completa cds//2.1e-47:294.89//Hs.3094:D31884
20 R-MAMMA1001711//ESTs//2.4e-86:439.96//Hs.18498:N52088
R-MAMMA1001715//ESTs//1.2e-73:399.9311:Hs.124620:AI082338
R-MAMMA1001730//ESTs//1.1e-85:403.99//Hs.125464:AI084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552.96//Hs.6923:
AI161158
25 R-MAMMA1001740//ESTs//4.6e-45:342.82//Hs.37573:H59651
R-MAMMA1001743//EST//2.7e-58:412.85//Hs.149742:AI285666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374.84//Hs.137041:AA877817
R-MAMMA1001751//EST//3.5e-36:375.73//Hs.139715:N25041
30 R-MAMMA1001754//EST//0.18:144.66//Hs.71957:AA151413
R-MAMMA1001757//ESTs//1.0e-9.8:488.96//Hs.45184:C14904
R-MAMMA1001760//ESTs//8.7e-29:206.86//Hs.143310:AI142276
R-MAMMA1001764//ESTs//0.00012:434.58//Hs.120051:AA707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299.85//Hs.149323:AB002325
35 R-MAMMA1001769//EST//1.7e-15:139.81//Hs.162399:AA572825
R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257.91//Hs.7634:
AA481246
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272.86//
Hs.73614:U83460
40 R-MAMMA1001785//ESTs//1.5e-87:431.98//Hs.131065:AA972238
R-MAMMA1001788//EST//0.95:108.62//Hs.145881:AI274644
R-MAMMA1001790//ESTs//4.0e-41:340.80//Hs.158045:AA425744
R-MAMMA1001806//EST//1.4e-40:297.84//Hs.141240:H60313
R-MAMMA1001812//ESTs//2.4e-93:446.98//Hs.129034:AA776892
45 R-MAMMA1001815//EST//0.00053:371.59//Hs.133255:AI052659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, completa cds//2.1e-46:325.87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303.89//Hs.149580:AI281881
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438.75//Hs.32567:AF073519
50 R-MAMMA1001836//ESTs//3.8e-06:128.71//Hs.143611:M78140
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339.83//Hs.43681:AL022394
R-MAMMA1001848//ESTs//2.1e-16:125.85//Hs.161662:AA836811
R-MAMMA1001851//ESTs//4.5e-48:344.84//Hs.138856:H47461
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280.83//Hs.155464:AF088219
55 R-MAMMA1001858//ESTs//1.1e-44:331.83//Hs.44702:AI148840
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262.77//Hs.5737:
AB007944
R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450.58//Hs.132206:

AF039694
R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//
Hs.73614:U83460
R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942
5 R-MAMMA1001880//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-
26:230:79//Hs.106008:AA147606
R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788
R-MAMMA1001907//Kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,
antigen detected by monoclonal and antibody I44))//6.7e-46:283:89//Hs.103458:X53795
10 R-nnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:A/251374
R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801
R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:
AB014606
R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790
15 R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506:
AA308018
R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734
R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084
R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219
20 R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054
R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.
154069:U06452
R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223
R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412
25 R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519
R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.
10458:AF088219
R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881
R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979
30 R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC
REGION [Bacillus subtilis]//4.0e-45:404:7811Hs/138596:N38806
R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875
R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:
AB013924
35 R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390
R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907
R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347
R-MAMMA1002118
R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081
40 R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//
Hs.129735:AF010144
R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:
AF035835
R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276
45 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886
R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548
R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503
R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:
AJ224162
50 R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040
R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509
R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638
R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.
92381:AB007956
55 R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734
R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038
R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:
AB014540

R-MAMMA1002230//Human 53K Isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP_K) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696
R-MAMMA1002236
R-MAMMA1002243
5 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0487//1.6e-54:207:81//Hs.92381:AB007956
R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283
R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772
10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141
R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751
R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:
AI275982
R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881
15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454
R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153
R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
2.3e-58:346:91//Hs.140385:AA773359
R-MAMMA1002308
20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.
154069:U06452
R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:
25 AF057280
R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317
30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618
R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:HS7439
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228
35 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
R-MAMMA1002356//Clathrin, light polypeptide (Lcb) //4.9e-31:217:88//Hs.73919:X81637
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
40 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
2.6e-30:244:81//Hs.129727:AF035587
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
R-MAMMA1002384//Small inducible cytokine A5 (RANTES) //1.8e-42:298:84//Hs.155464:AF088219
45 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:
83//Hs.86188:D87845
R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294
R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.
50 115325:D84488
R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588
R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477
R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H6475
R-MAMMA1002434//ESTs, Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]//
55 2.5e-106:521:98//Hs.112152:AA487348
R-MAMMA1002446//ESTs, Weakly similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//4.7e-
37:374:68//Hs.1517142:U85996
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

89121:AB007954
R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076
R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106
5 R-MAMMA1002475//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:
263:79//Hs.38687:AA744496
R-MAMMA1002487//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:
159:79//Hs.133526:N21103
R-MAMMA1002485//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:
10 AF055460
R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293
R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:
U07664
R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA808277
15 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//
3.9e-103:529:95//Hs.18858:AF065214
R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:
AB011147
R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
20 R-MAMMA1002556//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:
280:65//Hs.12725:T65056
R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433
25 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258
R-MAMMA1002597//Cytochrome P450, subfamily IB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//
Hs.1360:M29874
R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369
R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:
75//Hs.1361:M55053
R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670
35 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.
9332:AA811920
40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.
115325:D84488
R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390
R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
45 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
R-MAMMA1002655
R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886
R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087
R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-108:544:
50 96//Hs.16464:W19606
R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:
D86987
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385
55 R-MAMMA1002689//ESTs//5.9e-43:292:85//Hs.144660:AA652675
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510
R-MAMMA1002701//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:
353:96//Hs.138404:R70986

R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234
 R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858
 R-MAMMA1002721//*Homo sapiens* DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333
 R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571
 5 R-MAMMA1002728//Smad inducible cytokine A5 (RANTES)/3.4e-42:266:88//Hs.155464:AF088219
 R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757
 R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.
 154069:U06452
 10 R-MAMMA1002754//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//4.5e-40:
 369:77//Hs.105292:AA504776
 R-MAMMA1002758
 R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281
 R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651
 15 R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272
 R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750
 R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145
 R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812
 R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198
 20 R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260
 R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319
 R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881
 R-MAMMA1002835
 R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723
 25 R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395
 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238
 R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081
 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067
 R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941
 30 R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592
 R-MAMMA1002880//ESTs//6.5e-40:506:96//Hs.163533:N52194
 R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871
 R-MAMMA1002886//Small inducible cytokine A5 (RANTES)/3.4e-36:228:88//Hs.155464:AF088219
 R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA242811
 35 R-MAMMA1002890//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEESB82F [*C.elegans*]//4.2e-92:438:
 99//Hs.155871:AA533783
 R-MAMMA1002892//*Homo sapiens* EV15 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915
 R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087
 R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179
 40 R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002
 R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881
 R-MAMMA1002938
 R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503
 R-MAMMA1002947//ESTs//7.0e-22:220:80//Hs.103395:T79243
 45 R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353
 R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081
 R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630
 R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H158335
 R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279
 50 R-MAMMA1002987//*Homo sapiens* DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//
 2.1e-41:402:67//Hs.133089:AF064019
 R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179
 R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857
 R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R96117
 55 R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [*Rattus norvegicus*]//1.4e-53:320:90//Hs.
 92023:AI022248
 R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189
 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315
 R-MAMMA1003031//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358
 5 R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321
 R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160
 R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940
 R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941
 R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862
 10 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348
 R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881
 R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559
 R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:
 AA878911
 R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969
 15 R-MAMMA1003089//ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA4493652
 R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651
 R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283
 R-MAMMA1003113//EST//3.7e-28:457:70//Hs.123616:AA815366
 20 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788
 R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA866125
 R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537
 R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:
 L20861
 25 R-nnnnnnnnnnnn
 R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//
 Hs.6884:W30736
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640
 R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312
 30 R-NT2RM4000027
 R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663
 R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169
 R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds//4.0e-113:549:97//Hs.95665:
 35 AF070639
 R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817
 R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708
 R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312
 R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]
 40 //1.9e-99:536:92//Hs.127810:AI246301
 R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397
 R-nnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962
 R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160
 R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113
 45 R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723
 R-NT2RM400019911ESTs//10.020:95:6511Hs.146203:AI254528
 R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876
 R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.11138:
 50 AB018255
 R-NT2RM4000215
 R-nnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760
 R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor
 receptor) //0.00020:174:66//Hs.235:X51602
 55 R-NT2RM4000244//ESTs//8.6e-61:320:95//Hs.108646:AA613031
 R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein) //0.63:219:62//Hs.
 119498:AF000974
 R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

R-NT2RM4000280//ESTs//4.0e-87:435.96//Hs.162592:AA594128
 R-NT2RM4000324//ESTs//2.2e-80:413.96//Hs.12313:R43673
 R-NT2RM4000327//Small inducible cytokine A5 (RANTES)/(3.2e-45:286.87//Hs.155464:AF088219
 R-NT2RM4000344//Clathrin, light polypeptide (Lcb)/(8.6e-60:452.84//Hs.73919:X81637
 5 R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]/(2.5e- 117:57:96//Hs.5216:AA534881
 R-NT2RM4000354//ESTs//(2.1e-85:406.99//Hs.126774:AI224479
 R-NT2RM4000356//ESTs//(7.9e-109:548.96//Hs.44278:AA418063
 R-NT2RM4000366//Home sapiens mRNA for KIAA0642 protein, partial cds/(2.8e-113:577:95//Hs.8152:AB014542
 R-NT2RM4000368//ESTs//(2.2e-61:310.97//Hs.143611:M78140
 10 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//(1.0e-93:521.92//Hs.41793:
 AA775879
 R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//(1.9e-99:524.94//Hs.5249:U55977
 R-NT2RM4000414//EST//2.7e-06:196.64//Hs.136648:AA688285
 15 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//(5.4e-75:470.90//Hs.69235:
 AA192359
 R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112.69//Hs.19949:X98173
 R-NT2RM4000433//ESTs//(2.7e-100:479.98//Hs.24553:A150687
 R-NT2RM4000457//ESTs//(5.1e-107:535.95//Hs.7579:AA775865
 20 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//(6.0e-99:
 492.96//Hs.21090:AA418587
 R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//(2.2e-102:493.97//Hs.
 111279:WB4558
 R-NT2RM4000496
 25 R-NT2RM4000511//EST//5.1e-43:326.81//Hs.157658:AI358465
 R-NT2RM4000514//ESTs//(1.7e-112:552.96//Hs.6686:AA205496
 R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//(1.4e-60:343.93//Hs.16014:AA074879
 R-NT2RM4000520//ESTs//(2.7e-55:266.100//Hs.99838:AA204731
 30 R-NT2RM4000531//ESTs//(2.0e-88:502.91//Hs.13110:T67461
 R-NT2RM4000532//ESTs//(4.7e-290:58//Hs.148753:T91777
 R-NT2RM4000534//EST//0.00025:303.60//Hs.162809:AA632198
 R-NT2RM4000585//EST//0.28:63.77//Hs.150024:AI291981
 R-NT2RM4000590//ESTs//(5.8e-65:320.98//Hs.116017:AA613437
 35 R-NT2RM4000595//Home sapiens KIAA0431 mRNA, partial cds/(0.99:189:64//Hs.16349:AB007891
 R-NT2RM4000603//ESTs//(4.6e-68:356.96//Hs.48855:AA134589
 R-nnnnnnnnnnnn//ESTs//(1.5e-89:431.97//Hs.26117:W16697
 R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//(1.4e-102:
 519.96//Hs.14779:NG4822
 40 R-NT2RM4000674//ESTs//(5.1e-78:398.97//Hs.8268:N70144
 R-NT2RM4000689//ESTs, Weakly similar to T01G.4 [C.elegans]//(2.9e-115:550.98//Hs.11820:AA205531
 R-NT2RM4000698//ESTs//(2.0e-17:130:87//Hs.86420:AA927510
 R-nnnnnnnnnnnn
 R-NT2RM4000712//EST//0.99:103.65//Hs.114039:AA701128
 45 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
 //2.2e-103:519.95//Hs.6823:W18181
 R-NT2RM4000733//ESTs//(8.7e-88:429.98//Hs.72185:AA465311
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds/(3.6e-105:536.95//Hs.137168:
 AB018303
 50 R-NT2RM4000741//ESTs//(0.99:266.58//Hs.142718:AA034046
 R-NT2RM4000751//ESTs//(1.6e-20:351.66//Hs.43145:AA776988
 R-NT2RM4000764
 R-NT2RM4000778//EST//0.066:254.61//Hs.148232:AA904174
 R-NT2RM4000779//Home sapiens mRNA for KIAA0451 protein, complete cds/(9.3e-106:546.94//Hs.18586:
 55 AB007920
 R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//(6.5e-40:424.73//Hs.
 154069:U06452
 R-NT2RM4000790//EST//9.0e-48:259.94//Hs.159694:AI417008

R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0.203.63//Hs.20991:D31891
 R-NT2RM4000796//ESTs//7.0e-106:506.98//Hs.43559:AI003520
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158.96//Hs.118249:
 M21868
 5 R-NT2RM4000813
 R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539.97//Hs.99636:
 AI219667
 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448.99//Hs.20223:AA482031
 R-NT2RM4000848//ESTs//8.1e-97:476.97//Hs.16036:AA883864
 10 R-NT2RM4000852//ESTs//6.4e-94:467.97//Hs.11556:AI309597
 R-NT2RM4000855//ESTs//2.9e-95:544.90//Hs.106525:AI283343
 R-nnnnnnnnnnnn
 R-NT2RM4000895//ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//9.3e-
 96:450.99//Hs.142076:AA604514
 15 R-NT2RM4000950//ESTs//2.6e-99:41.98//Hs.43827:AA455262
 R-NT2RM4000971//EST//2.9e-96:461.99//Hs.139709:AA227887
 R-NT2RM4000979//EST//1.6e-97:329.98//Hs.96927:AA349647
 R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414.96//Hs.115342:
 AA650126
 20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545.97//Hs.19542:
 AB018272
 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556.97//Hs.15711:
 AB014539
 R-NT2RM4001032//ESTs//7.8e-17:132.84//Hs.138720:N53352
 25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133.67//Hs.
 32170:AB015132
 R-NT2RM4001054//ESTs//1.7e-84:404.99//Hs.116407:AA815300
 R-nnnnnnnnnn//ESTs//3.4e-91:439.99//Hs.103177:W72798
 R-NT2RM4001092//ESTs//1.4e-86:517.8911Hs.132969:Z78324
 30 R-NT2RM4001116//EST//5.2e-57:275.100//Hs.131115:AI016962
 R-NT2RM4001140//ESTs//5.5e-96:461.98//Hs.86965:AA252276
 R-NT2RM4001151//ESTs//0.40:263.58//Hs.113189:R08311
 R-NT2RM4001155//ESTs//8.3e-105:544.94//Hs.29647:W60848
 R-NT2RM4001160//EST//7.6e-25:380.68//Hs.147405:AI209085
 35 R-NT2RM4001187//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//9.2e-
 43:273.91//Hs.109005:N31174
 R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase) //3.1e-32:274.70//Hs.2379:U23942
 R-NT2RM4001200//ESTs//4.5e-102:494.97//Hs.31844:N32849
 R-NT2RM4001203
 40 R-NT2RM4001204//ESTs//9.8e-88:468.93//Hs.4990:T65307
 R-NT2RM4001217//ESTs//1.2e-75:396.94//Hs.25042:R72410
 R-NT2RM4001256//ESTs//1.0:157.62//Hs.65377:AA994677
 R-NT2RM4001258//ESTs//9.6e-41:260.88//Hs.27633:N76184
 R-NT2RM4001309
 45 R-NT2RM4001313//EST//0.0022:150.66//Hs.161573:W84857
 R-NT2RM4001316//ESTs//3.5e-26:139.99//Hs.23100:AI128899
 R-NT2RM4001320//ESTs//1.6e-97:308.99//Hs.112024:AI042352
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522.97//Hs.
 18442:AI129307
 50 R-NT2RM4001344//EST//1.1e-90:436.99//Hs.95900:AA160339
 R-NT2RM4001347//EST//0.17:186.61//Hs.16751:T80476
 R-NT2RM4001371//EST//0.0069:270.62//Hs.99239:AA450211
 R-NT2RM4001382
 R-NT2RM4001384//ESTs//9.6e-91:445.98//Hs.55000:AA805507
 55 R-NT2RM4001410//EST//0.13:50.82//Hs.157675:AI358790
 R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:
 94//Hs.15744:AI055859
 R-NT2RM4001412

- R-NT2RM4001414//ESTs//6.5e-35:226.88//Hs.121727:AA775895
 R-NT2RM4001437//EST/0.017:169.67//Hs.13207:F10054
 R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544.94//Hs.7558:AA526812
 5 R-NT2RM4001454//ESTs//4.7e-108:517.98//Hs.32295:N32277
 R-NT2RM4001455//EST/9.6e-81:395.97//Hs.129798:AA969739
 R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324.85//Hs.22271:D26067
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547.93//Hs.153121:
 AB014585
 10 R-NT2RM4001519//Histatin 1//0.53:340.59//Hs.119101:M26664
 R-NT2RM40015227//Small inducible cytokine A5 (RANTES)//8.4e-55:306.80//Hs.155464:AF088219
 R-NT2RM4001557//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165.83//Hs.29134:H43072
 R-NT2RM4001565//ESTs//2.0e-103:483.99//Hs.121273:AA758027
 R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase)LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446.72//Hs.4943:Z98046
 15 R-NT2RM4001569//ESTs//3.6e-37:186.100//Hs.86959:AA888009
 R-NT2RM4001582//ESTs//1.2e-96:459.98//Hs.114432:N52946
 20 R-nnnnnnnnnnnn
 R-NT2RM4001594//ESTs//1.6e-83:404.98//Hs.134740:AA282171
 R-NT2RM4001597//ESTs//6.9e-111:558.96//Hs.11408:AI358871
 R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565.95//Hs.23255:
 AB018334
 25 R-NT2RM4001611//EST//5.9e-74:353.99//Hs.125318:AA837079
 R-NT2RM4001629//ESTs//6.1e-95:453.99//Hs.115765:AA485957
 R-NT2RM4001650
 R-NT2RM4001662
 R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230.70//Hs.7764:
 30 AB007938
 R-NT2RM4001682//EST//4.3e-68:393.90//Hs.157362:AI367496
 R-NT2RM4001710//ESTs//4.3e-48:235.99//Hs.7299:AA203440
 R-NT2RM4001714//ESTs//0.0014:568.58//Hs.50458:AA868686
 R-nnnnnnnnnnnn//ESTs//6.5e-104:487.99//Hs.153581:AA630465
 35 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563.94//Hs.18510:
 AA522887
 R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124.68//Hs.
 120980:S83390
 R-NT2RM4001746//ESTs//6.1e-90:420.100//Hs.139003:AA948200
 40 R-NT2RM4001754//Human kpnl repeat mrna (cdna clone pcd-kpnl-4), 3' end//5.4e-59:504.78//Hs.139107:K00629
 R-NT2RM4001758//ESTs//8.9e-27:140.100//Hs.149973:AI290740
 R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236.80//Hs.39871:AB018270
 R-NT2RM4001783//ESTs//9.9e-30:156.99//Hs.115260:AA314956
 R-NT2RM4001810//ESTs//1.3e-65:346.95//Hs.139115:W22567
 45 R-NT2RM4001813//ESTs//5.7e-102:473.100//Hs.87574:AI089920
 R-NT2RM4001823//ESTs//3.8e-62:324.95//Hs.124109:AA888839
 R-NT2RM4001828//ESTs//1.3e-119:563.98//Hs.102397:AA706551
 R-NT2RM4001836//ESTs//5.5e-16:92.100//Hs.26996:AA551070
 R-NT2RM4001841//ESTs//1.3e-99:540.94//Hs.42322:AA082819
 50 R-NT2RM4001842//ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//4.1e-10:
 274.62//Hs.161959:AA493652
 R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-
 43:292.86//Hs.14202:N46000
 R-nnnnnnnnnnnn//ESTs//6.2e-104:495.98//Hs.118686:AA682280
 55 R-NT2RM40018657//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592.97//Hs.61628:
 Y17711
 R-NT2RM4001876//ESTs//2.9e-98:532.92//Hs.100734:AA158252
 R-NT2RM4001880//ESTs//2.5e-29:224.86//Hs.6193:AA045149

R-NT2RM4001905//ESTs/[5.6e-109:565:95//Hs.9536:AA114178
R-NT2RM4001922//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:
535:95//Hs.30991:AA994438
R-NT2RM4001930//ESTs/[4.1e-84:425:96//Hs.80042:N63143
5 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:
AF098162
R-NT2RM4001953//ESTs/[5.3e-65:338:96//Hs.33718:AA453268
R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
10 R-nnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097
R-NT2RM4001979//ESTs/[1.4e-96:465:98//Hs.157103:W60265
R-NT2RM4001984
R-NT2RM4001987
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528
15 R-NT2RM4002018
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087
R-NT2RM4002044//ESTs/[2.8e-107:537:96//Hs.24078:W44435
R-NT2RM4002054//ESTs/[3.7e-88:482:94//Hs.4243:T78226
R-NT2RM4002062//ESTs/[1.4e-55:377:85//Hs.152592:AA587887
20 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179
R-nnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:
AF071309
R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629
R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//
25 Hs.109274:AA193416
R-NT2RM4002075//ESTs/[0.078:267:61//Hs.163563:AA641655
R-NT2RM4002093//ESTs/[1.2e-64:316:99//Hs.34956:AI052528
R-nnnnnnnnnnnn//ESTs/[1.0e-95:69//Hs.25897:W65409
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620
30 R-NT2RM4002140//ESTs/[5.6e-46:187:94//Hs.8737:W22712
R-NT2RM4002145//ESTs/[4.6e-70:374:94//Hs.141082:H18987
R-NT2RM4002146//ESTs/[1.9e-93:43:9:99//Hs.119295:AA442090
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258
35 R-NT2RM4002189//ESTs/[9.6e-75:352:100//Hs.98350:H15400
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:A/244343
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
R-NT2RM4002213//ESTs/[3.3e-15:160:78//Hs.63304:W22079
R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]
40 //5.1e-112:569:95//Hs.23900:U82984
R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglu-
cosaminyltransferase [C.elegans]/1.1e-100:544:93//Hs.27567:W72190
R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219
R-NT2RM4002266//ESTs/[2.6e-100:539:95//Hs.57978:AA535864
45 R-NT2RM4002278//ESTs/[1.8e-112:569:95//Hs.87281:AA128263
R-NT2RM4002281//ESTs/[4.9e-20:187:80//Hs.141203:H52638
R-NT2RM4002287//ESTs/[7.9e-84:388:94//Hs.33977:NS2461
R-NT2RM4002294
R-NT2RM4002301//ESTs/[4.5e-111:556:96//Hs.85916:AA194164
50 R-NT2RM4002323//ESTs/[4.5e-102:498:97//Hs.85782:AA191498
R-nnnnnnnnnnnn//ESTs/[5.0e-59:283:100//Hs.125048:AA682913
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:
AB014549
55 R-NT2RM4002374//ESTs/[3.3e-40:505:70//Hs.951175:AA206594
R-NT2RM4002383//ESTs/[2.7e-93:455:97//Hs.134278:AA648884
R-NT2RM4002390//ESTs/[3.3e-93:481:95//Hs.48764:AA613328
R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

98/Hs.16464:W19606
R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677
R-NT2RM4002446
R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142
5 R-NT2RM4002457
R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890
R-NT2RM4002479//*Homo sapiens* RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.
8765:AF083255
R-NT2RM4002482//*Homo sapiens* mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:
10 AB014591
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884
R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029
R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464
R-nnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [*H.sapiens*]//1.4e-73:360:91//
15 Hs.31030:H50467
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788
R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057
R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312
R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE [Bos
20 taurus]//2.3e-89:435:97//Hs.15830:AA165698
R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569
R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [*Thermus aquaticus thermophilus*]
//9.6e-28:194:87//Hs.59346:AI126802
R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096
25 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081
R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115
R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713
R-NT2RP2000040//*Homo sapiens* mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290
R-NT2RP2000045//*Homo sapiens* tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//
30 4.3e-64:309:98//Hs.6216:AF061749
R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910
R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [*D.melanogaster*]//2.3e-35:199:94//Hs.41793:
AA775879
35 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [*R.norvegicus*]//1.4e-78:383:98//Hs.58254:W72881
R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097
R-NT2RP2000077//*Homo sapiens* growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.
54877:AF050078
R-NT2RP2000079//*Homo sapiens* RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.
40 102576:AJ010230
R-NT2RP2000088//*Homo sapiens* mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338
R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064
R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757
R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827
45 R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419
R-NT2RP2000114//*Homo sapiens* mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356
R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
[C.elegans]//1.9e-19:153:86//Hs.5268:W22670
R-nnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099
50 R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356613
R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [*Mus musculus*]//3.0e-
89:457:95//Hs.3832:AI208601
R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548
R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA04020
55 R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:AI188190
R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741
R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373
R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897
 R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382
 R-NT2RP2000232
 5 R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683
 R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379
 R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005
 R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840
 10 R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649
 R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:AI261382
 R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635
 R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865
 15 R-NT2RP2000289
 R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249
 R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712
 R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:
 20 93//Hs.58218:U82381
 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3..41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398
 25 R-NT2RP2000329//ESTs, Highly similar to GTP-AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441
 R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062
 R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:
 94//Hs.76556:UB3981
 30 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103
 R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010
 R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324
 R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:
 90//Hs.5819:AF102265
 35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425
 R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045
 R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013
 R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078
 40 R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215
 R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896
 R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348
 R-NT2RP2000523
 R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144
 45 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446
 R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514
 R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222
 R-NT2RP2000656//ESTs//1.0e-128:80//Hs.23977:AA115275
 R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396
 50 R-NT2RP2000668//ESTs//2.2e-40:255:88//Hs.113310:R16767
 R-NT2RP2000678//ESTs//2.6e-53:271:961:1Hs.23790:N99347
 R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368
 R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279
 R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965
 55 R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:NG2642
 R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419
 R-NT2RP2000809
 R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

R-nnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404
 R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918
 R-NT2RP2000819
 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511
 5 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165
 R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552
 R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345
 R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:
 10 AB018284
 R-NT2RP2000892//ESTs//2.8e-50:25:8:96//Hs.119238:AA476267
 R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266
 R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477
 15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:AB018298
 R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021
 R-NT2RP2000970//EST//8.7e-06:255:62//Hs.149202:AI246481
 R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 98.6 KD PROTEIN IN SIS2-MTD1 INTERGENIC
 20 REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537
 R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521
 R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643
 R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660
 R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108
 25 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665
 R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068
 R-NT2RP2001119
 R-NT2RP2001127//Homo sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348
 R-NT2RP2001137
 30 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512
 R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145
 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:
 AB007949
 R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287
 35 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510
 R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402
 R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358
 R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//
 Hs.44014:AA632298
 40 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996
 R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353
 R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229
 R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775
 R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.47305:AA12665
 45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7981:AA401205
 R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//
 2.3e-43:238:93//Hs.106632:N25679
 R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138
 R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178
 50 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028
 R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038
 R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.
 sapiens]//3.9e-74:411:93//Hs.47305:AA195153
 R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875
 55 R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:
 469:97//Hs.20483:AA522505
 R-NT2RP2001420//ESTs//1.1e-49:228:88//Hs.163602:N32030
 R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

R-NT2RP2001427//EST//1.7e-1 1.107.84//Hs.148584:AI201728
 R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114.558.97//Hs.7627:AI341556
 R-NT2RP2001440//EST//0.17.192.58//Hs.133442:AI061394
 R-NT2RP2001445//ESTs//1.1e-43.215.100//Hs.145497:AA501453
 5 R-NT2RP2001449//ESTs//4.1e-08.234.61//Hs.134067:AI076765
 R-NT2RP2001450//ESTs//9.5e-65.356.94//Hs.61829:AI079539
 R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34.255.83//Hs.155464:AF088219
 R-NT2RP2001506//ESTs//2.9e-23.170.88//Hs.7147:T23513
 R-NT2RP2001511//ESTs//2.0e-08.59.100//Hs.57660:AA251146
 10 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106.545.95//Hs.4277:Y14494
 R-NT2RP2001526//ESTs//3.7e-23.295.72//Hs.8514:AF039240
 R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15.99.95//Hs.99742:AF035566
 15 R-NT2RP2001560//ESTs//2.2e-58.310.94//Hs.87454:AA732816
 R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76.387.96//Hs.67619:AB007957
 R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17.193.60//Hs.119:D14661
 R-NT2RP2001581//ESTs//5.1e-08.107.78//Hs.157114:T58884
 20 R-NT2RP2001597//EST//5.2e-22.151.88//Hs.158613:AI369995
 R-NT2RP2001601//ESTs//1.5e-78.373.99//Hs.137558:AI393767
 R-NT2RP2001613
 R-NT2RP2001628//EST//0.99.195.60//Hs.144238:W52294
 R-NT2RP2001663//ESTs//4.0e-37.282.84//Hs.12319:W56090
 25 R-NT2RP2001677//ESTs//1.4e-44.232.96//Hs.159387:AI370845
 R-NT2RP2001678//ESTs//0.91.124.60//Hs.10593:AI201336
 R-NT2RP2001699//EST//0.0033.230.61//Hs.146544:AI125323
 R-NT2RP2001720//ESTs//1.8e-52.255.99//Hs.101064:AA290579
 R-NT2RP2001721//ESTs//7.0e-101.479.99//Hs.129750:AA987538
 30 R-NT2RP2001740//ESTs//3.3e-76.379.96//Hs.144704:AI147100
 R-NT2RP2001748//ESTs//1.4e-44.352.81//Hs.142259:AA828840
 R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105.519.96//Hs.47504:
 AF091754
 R-NT2RP2001813//ESTs//6.3e-78.406.95//Hs.21902:R44037
 35 R-NT2RP2001861
 R-NT2RP2001869//EST//2.8e-21.173.82//Hs.130321:AI002941
 R-NT2RP2001876//ESTs//6.1e-102.526.95//Hs.4944:AA533088
 R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110.556.95//Hs.23159:
 AA113849
 40 R-NT2RP2001900//ESTs//6.9e-85.442.95//Hs.154220:AA171724
 R-NT2RP2001907//ESTs//2.1e-82.432.94//Hs.142257:AA188423
 R-NT2RP2001926//EST//2.3e-24.299.71//Hs.135085:AI097268
 R-NT2RP2001936//ESTs//1.1e-45.265.92//Hs.112482:T66087
 R-NT2RP2001943//EST//1.0e-05.246.61//Hs.144096:AI032180
 45 R-NT2RP2001946//ESTs//3.6e-87.410.99//Hs.202422:WT2594
 R-NT2RP2001947//ESTs//1.9e-55.338.88//Hs.58582:T72588
 R-NT2RP2001969
 R-NT2RP2001976//ESTs//1.2e-98.499.95//Hs.121028:AA902745
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15.118:
 50 89//Hs.18760:AA166678
 R-NT2RP2002025//ESTs//2.1e-82.393.98//Hs.159488:AI378233
 R-NT2RP2002032//ESTs//4.4e-98.531.91//Hs.93836:AA813332
 R-NT2RP2002033//ESTs//3.5e-43.229.96//Hs.30563:AA102627
 R-NT2RP2002041
 55 R-NT2RP2002046//ESTs//1.6e-101.476.99//Hs.101107:AA825938
 R-NT2RP2002047//ESTs//9.1e-85.431.95//Hs.116750:AA629895
 R-NT2RP2002058//ESTs//1.3e-31.163.99//Hs.33085:AA258068
 R-NT2RP2002066//ESTS//1.9e-87.459.93//Hs.118871:AA846091

R-NT2RP2002070//ESTs//4.1e-63:332.98//Hs.156446:T92265
 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178.87//Hs.11039:AF052183
 R-NT2RP2002079//ESTs//1.2e-79:389.97//Hs.135214:AI350524
 R-NT2RP2002089//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376.89//Hs.155218:
 5 AJ007509
 R-NT2RP2002104//ESTs//8.4e-54:313.90//Hs.98702:AI123000
 R-NT2RP2002124//ESTs//6.6e-81:431.93//Hs.127326:AA525134
 R-NT2RP2002137//Deoxyctydine kinase//0.29:183.62//Hs.709:M60527
 R-NT2RP2002154//ESTs//9.6e-97:539.91//Hs.18624:AA523268
 10 R-NT2RP2002172//EST//0.69:53.75//Hs.156238:AI334495
 R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269.98//Hs.107201:W52859
 R-NT2RP2002192//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.9e-
 15 15:245.71//Hs.87578:AI125363
 R-NT2RP2002193//ESTs//3.7e-79:45.39//Hs.76578:AI290672
 15 R-NT2RP2002208//ESTs//2.0e-72:347.99//Hs.164028:AI003946
 R-NT2RP2002219//EST//0.039:229.63//Hs.149830:AI287499
 R-NT2RP2002231//ESTs//3.3e-64:337.94//Hs.79828:AA642341
 R-nnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238.99//Hs.22583:
 AA188168
 20 R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131.83//Hs.150595:
 AF005418
 R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548.91//Hs.92137:M19720
 R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550.91//Hs.4029:Z78373
 R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482.93//Hs.5570:AI377863
 25 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527.94//
 Hs.24812:AF069532
 R-NT2RP2002316//ESTs//4.2e-91:425.100//Hs.3350:AI368015
 R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:
 95//Hs.31034:AB015594
 30 R-NT2RP2002333//ESTs//1.9e-86:483.91//Hs.155198:AA767372
 R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:
 89//Hs.109051:AF038958
 R-NT2RP2002394//ESTS//0.11:158.65//Hs.28792:AI343467
 R-NT2RP2002408//ESTs//1.5e-51:278.93//Hs.6044:W22815
 35 R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285.80//Hs.15731:
 AB011135
 R-NT2RP2002439//ESTS//3.2e-12:134.76//Hs.32246:AA464020
 R-NT2RP2002457//ESTs//4.7e-52:282.94//Hs.21968:H97521
 R-NT2RP2002464//ESTs//5.3e-27:148.98//Hs.115660:AI362230
 40 R-NT2RP2002475//ESTs//3.9e-85:439.94//Hs.9873:W27233
 R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605.92//Hs.
 125856:AB005289
 R-NT2RP2002498//ESTs//6.3e-37:227.93//Hs.108779:N73180
 R-NT2RP2002503//ESTs//1.9e-54:358.86//Hs.57800:W60388
 45 R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583.91//Hs.23255:
 AB018334
 R-NT2RP2002520//ESTs//4.2e-99:509.94//Hs.32368:AA205305
 R-NT2RP2002537//ESTs//4.2e-105:552.93//Hs.154363:AA533090
 R-NT2RP2002546//Homo sapiens clone TUAB Cri-du-chat region mRNA//2.6e-109:570.93//Hs.49476:AF009314
 50 R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189.86//Hs.80961:U60325
 R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564.97//Hs.94549:
 AA149547
 R-NT2RP2002595//EST//1.4e-15:101.95//Hs.129528:AA994783
 R-NT2RP2002606//ESTs//4.5e-99:475.98//Hs.45046:N40170
 55 R-NT2RP2002609//ESTs//1.9e-104:568.92//Hs.9175:AI184220
 R-NT2RP2002618//ESTs//0.014:493.57//Hs.96322:AA541615
 R-NT2RP2002621//EST//4.4e-36:252.84//Hs.149580:AI281881
 R-NT2RP2002643//ESTs//6.9e-32:247.74//Hs.33354:AI179944

R-NT2RP2002672
R-NT2RP2002701//N-acetylglucosaminidase, alpha- [Sanfilippo disease IIIB]/0.99:184:63//Hs.50727:U43572
R-NT2RP2002706//ESTs/2.8e-41:148:86//Hs.161917:AA483223
R-NT2RP2002710//ESTs/0.34:105:71//Hs.136747:AA749210
5 R-NT2RP2002727//ESTs/8.7e-68:368:94//Hs.14366:T78626
R-NT2RP2002736//ESTs/9.7e-98:457:99//Hs.74899:AA993300
R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108
R-NT2RP2002741//ESTs/3.1e-102:489:98//Hs.112024:AI042352
R-NT2RP2002750//ESTs/3.6e-43:166:86//Hs.162404:AA571311
10 R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042
R-NT2RP2002753//ESTs/1.7e-49:262:96//Hs.49005:W89124
R-NT2RP2002769//ESTs/1.3e-59:376:88//Hs.4046:H03587
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537
R-NT2RP2002800//ESTs/6.5e-08:79:84//Hs.153262:AA551124
15 R-NT2RP2002839//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578
R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031
R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870
R-NT2RP2002880
20 R-NT2RP2002891
R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894
R-NT2RP2002928//ESTs/3.9e-108:502:99//Hs.29105:AA574143
R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096
R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771
25 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480
R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060
R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213
R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//
Hs.106290:AI125291
30 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329
R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.
sapiens]//2.4e-98:467:98//Hs.86337:AA149311
R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
R-NT2RP2003034//ESTs/9.3e-87:408:96//Hs.164042:H12594
35 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082
R-NT2RP2003099//Thromboxane A2 receptor (g17) mRNA, complete cds//2.6e-42:328:81//Hs.89887:D38081
R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345
R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355
40 R-NT2RP2003125
R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
R-NT2RP2003137//ESTs//2.1e-37:258:85//Hs.63169:N78506
R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8986:AA629067
45 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
50 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438
R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937
R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859
R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-11:565:95//Hs.154919:
55 AB014525
R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321
 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
 R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553.96//Hs.26089:AA195126
 5 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
 R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618
 R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.15573:AI312825
 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA590914
 R-NT2RP2003391//ESTs//1.8e-98:484:97//Hs.5842:AA534476
 10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
 R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249
 R-NT2RP2003401//ESTs//8.1e-25:161:90//Hs.155360:AA984683
 R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.e-106:508:98//Hs.131840:AI016073
 15 R-NT2RP2003445//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360
 R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903
 R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332
 R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121
 20 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777
 R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831
 R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270
 25 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma virus (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783
 R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170
 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101
 R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684
 30 R-NT2RP2003559//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439
 R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696
 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719
 R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:
 35 AA126463
 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067
 R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981
 R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC
 40 REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188
 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951
 R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523
 R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:AI148540
 R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs.
 45 93332:AA811920
 R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097
 R-NT2RP2003713//EST//0.81:210:59//Hs.145517:T79401
 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003
 50 R-nnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914
 R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis el-
 egans]//2.4e-50:302:90//Hs.19196:W74577
 R-NT2RP2003751
 R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808
 55 R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709
 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:
 AF047437

R-NT2RP2003777//ESTs//2.6e-59:323.94//Hs.10101:AI381811
 R-NT2RP2003781//ESTs//2.0e-25:269.75//Hs.144951:N34836
 R-NT2RP2003793//ESTs//8.7e-94:466.97//Hs.93949:AA782955
 R-NT2RP2003840//ESTs//3.4e-97:533.93//Hs.16130:AA195077
 5 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351.65//Hs.75196:X69838
 R-NT2RP2003859//ESTs//3.0e-07:96.81//Hs.153262:AA551124
 R-NT2RP2003871//ESTs//1.9e-102:509.97//Hs.25726:AA430167
 R-NT2RP2003885//ESTs//1.0e-102:502.97//Hs.36353:AA702341
 R-NT2RP2003912//EST//1.2e-38:336.76//Hs.134975:AI094611
 10 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROCC-1B) mRNA, complete cds//0.90:190.60//Hs.75875:U49278
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568.97//
 Hs.35086:AB014458
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540.97//Hs.7302:
 15 AB007916
 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568.96//Hs.7316:AB018347
 R-NT2RP2003984
 R-NT2RP2003986//ESTs//4.9e-36:272.82//Hs.158268:AA738087
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519.99//Hs.36093:
 20 AI49968
 R-NT2RP2004014//ESTs//8.4e-102:483.99//Hs.22867:AI417478
 R-NT2RP2004041
 R-NT2RP2004042//ESTs//1.5e-105:466.97//Hs.7296:N29706
 R-nnnnnnnnnnnnnn//ESTs//1.4e-110:559.96//Hs.71916:AA219699
 25 R-NT2RP2004081//ESTs//3.7e-105:503.98//Hs.27542:AA977204
 R-NT2RP2004098//EST//7.3e-26:203.87//Hs.21897:RA41461
 R-NT2RP2004124//ESTs//1.1e-83:435.95//Hs.43299:N23036
 R-NT2RP2004142//EST//1.3e-06:165.65//Hs.146742:AI147500
 R-NT2RP2004152//ESTs//7.0e-98:455.100//Hs.17731:AI342241
 30 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:
 583.97//Hs.16520:AI224533
 R-NT2RP2004170//ESTs//6.7e-66:407.88//Hs.157138:AI348544
 R-NT2RP2004172//ESTs//1.5e-109:567.95//Hs.159091:AA033974
 R-NT2RP2004187//ESTs//3.6e-92:488.93//Hs.22954:W26589
 35 R-NT2RP2004194//ESTs//6.2e-114:585.95//Hs.18778:AA203167
 R-NT2RP2004196
 R-NT2RP2004207//ESTs//6.3e-102:488.98//Hs.22678:AA604756
 R-NT2RP2004226//ESTs//8.8e-18:252.71//Hs.11924:W26972
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499.98//Hs.143460:
 40 AA483305
 R-NT2RP2004239//ESTs//1.2e-16:171.80//Hs.16134:AA203116
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530.93//Hs.
 54900:AF039687
 R-NT2RP2004242//ESTs//1.3e-85:460.93//Hs.104535:AA211483
 45 R-NT2RP2004245//ESTs//6.4e-117:575.97//Hs.23744:AA035744
 R-NT2RP2004270//ESTs//1.0:95.69//Hs.141371:H92187
 R-NT2RP2004300//ESTs//4.4e-80:379.99//Hs.130874:AA905056
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544.96//Hs.61152:
 AF000416
 50 R-NT2RP2004321//ESTs//2.1e-18:104.99//Hs.107207:AA044788
 R-NT2RP2004339//EST//1.4e-47:309.86//Hs.161917:AA483223
 R-NT2RP2004347
 R-NT2RP2004364//ESTs//1.1e-113:566.96//Hs.25880:AI268173
 R-NT2RP2004365//ESTs//0.022:271.62//Hs.38897:AI129310
 55 R-NT2RP2004366//ESTs//9.5e-71:335.100//Hs.91867:AI218624
 R-NT2RP2004373//ESTs//4.2e-25:172.87//Hs.83243:N32192
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III
 [Caenorhabditis elegans]//1.4e-11:108.82//Hs.30490:AA146916

R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N679473
 R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921
 5 R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121
 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124
 R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds//
 8.6e-34:143:98//Hs.154729:AF017995
 10 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700
 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320
 R-NT2RP2004538//Thromboxane A2 receptor/1.4e-45:279:89//Hs.89887:D38081
 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347
 R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470
 15 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661
 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126
 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666
 R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862
 R-NT2RP2004602//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//4.5e-07:
 20 149.76//Hs.12845:N28835
 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587:96//Hs.5198:AJ006291
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:96//Hs.29956:
 AB007929
 25 R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930
 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:96//Hs.154919:
 AB014525
 R-NT2RP2004709//ESTs//1.1e-50:51:98//Hs.38034:AI149793
 30 R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AI203433
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:96//Hs.4236:
 AB007947
 R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015
 R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423
 35 R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774
 R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
 8.0e-116:564:96//Hs.40820:AF058953
 R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579
 40 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:
 AF054179
 R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906
 R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803
 R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567
 45 R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529
 R-nnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543
 R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941
 R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087
 50 R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496
 R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910
 R-NT2RP2004985
 R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902
 R-NT2RP2005000
 55 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:
 AB014515
 R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235
 R-nnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

R-NT2RP2005018//ESTs//7.5e-46:280.90//Hs.126857:AA932161
 R-NT2RP2005020//ESTs//1.6e-105:554.94//Hs.14846:AA148507
 R-NT2RP2005031//ESTs//3.1e-79:379.99//Hs.139709:AA227887
 R-NT2RP2005037//ESTs//5.3e-102:551.93//Hs.26516:AA195220
 5 R-NT2RP2005038//ESTs//5.8e-101:566.92//Hs.46964:N49757
 R-NT2RP2005108
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105.518.97//Hs.22616:
 AB014564
 R-NT2RP2005120//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464.85//Hs.
 10 100555:X98743
 R-NT2RP2005139//ESTs//1.0e-108:545.95//Hs.21006:AA523383
 R-NT2RP2005140//ESTs//4.3e-90:422.99//Hs.62180:A1341261
 R-NT2RP2005144//ESTs//0.91:162.62//Hs.52399:AI075744
 R-NT2RP2005147//ESTs//4.6e-100:502.96//Hs.27931:AA633438
 15 R-NT2RP2005159//ESTs//7.5e-105:533.95//Hs.109819:AI357582
 R-NT2RP2005162//ESTs//6.6e-83:419.96//Hs.113998:H50648
 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513.95//Hs.155218:
 AJ007509
 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-
 20 115.577.96//Hs.7600:H98166
 R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359.82//Hs.154103:AF061258
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:
 245.97//Hs.21090:AA418587
 R-NT2RP2005254//ESTs//3.3e-111:581.94//Hs.22549:AA524503
 25 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III
 [Caenorhabditis elegans]//1.1e-79:412.95//Hs.23047:N66596
 R-NT2RP2005276//ESTs//4.6e-85:426.96//Hs.24550:AA316272
 R-NT2RP2005287//ESTs//1.7e-109:565.94//Hs.61976:AI279001
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594.98//
 30 Hs.27007:AF060219
 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545.96//Hs.44766:AJ007590
 R-NT2RP2005293//ESTs//5.1e-116:538.99//Hs.62180:A1341261
 R-NT2RP2005315//ESTs//1.4e-82:415.97//Hs.155829:AA018338
 R-NT2RP2005325//Human LIM-homeobox domain protein (LHL-2) mRNA, complete cds//2.5e-45:272.91//Hs.
 35 1569:U11701
 R-NT2RP2005336//ESTs//1.9e-93:444.99//Hs.110966:AA151699
 R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFP) mRNA, complete cds//0.011:463:
 58//Hs.150926:AF017445
 R-NT2RP2005354//ESTs//7.2e-22:148.91//Hs.153783:H14544
 40 R-NT2RP2005360//ESTs//0.048:225.60//Hs.7602:AA099247
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248.82//Hs.93121:AB018304
 R-NT2RP2005407//ESTs, Weakly similar to OS11 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461.88//Hs.
 70849:AA121697
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II
 45 [C.elegans]//8.1e-96:491.95//Hs.7194:A185631
 R-NT2RP2005441//ESTs//1.1e-110:548.96//Hs.5209:AA780068
 R-NT2RP2005453//ESTs//0.94:352.58//Hs.25870:H14423
 R-NT2RP2005457//ESTs//2.1e-46:236.97//Hs.19522:AA975096
 R-NT2RP2005464//ESTs//1.8e-72:349.99//Hs.44045:N51307
 50 R-NT2RP2005465//ESTs//0.0058:322.58//Hs.127009:AI378936
 R-NT2RP2005472//ESTs//0.47:309.60//Hs.144838:AI22019
 R-NT2RP2005476//ESTS//5.1 e-40:205.9811Hs.101577:AI168526
 R-NT2RP2005490//ESTs//L3e-70:364.96//Hs.134382:AA083573
 R-NT2RP2005491//EST//0.012:220.60//Hs.144448:AA812455
 55 R-NT2RP2005495//ESTs//1.2e-86:501.91//Hs.99445:R53540
 R-NT2RP2005496//ESTs//3.2e-34:263.81//Hs.70279:AA757426
 R-NT2RP2005498//ESTS, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT,
 NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284.88//Hs.85752:AI138993

R-NT2RP2005501//ESTs//2.5e-84:404.98//Hs.143812:AI141755
 R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215.92//Hs.5298:AA725071
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:
 5 570:9411Hs.119023:AF092563
 R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:
 433.95//Hs.36942:AA524535
 R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560.94//Hs.159597:
 10 AJ012449
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583.96//Hs.62515:
 AB007963
 R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572
 R-NT2RP2005551//ESTs//8.6e-108:507.99//Hs.68613:AI357567
 15 R-NT2RP2005557//ESTs//3.1e-105:495.99//Hs.105985:AA885169
 R-NT2RP2005581//ESTs//1.7e-79:445.92//Hs.138152:H03240
 R-NT2RP2005600//ESTs//1.3e-38:192.100//Hs.48329:W92733
 R-NT2RP2005605//ESTs//7.6e-87:409.99//Hs.45005:AA975060
 R-NT2RP2005620//ESTs//2.9e-96:463.97//Hs.7407:AI376788
 20 R-NT2RP2005622//ESTs//1.8e-104:497.98//Hs.22595:AA394229
 R-NT2RP2005637//EST//2.5e-20:163.71//Hs.161164:AI418211
 R-NT2RP2005640//ESTs//5.0e-99:473.98//Hs.23467:AA708740
 R-NT2RP2005645//ESTs//9.5e-23:231.77//Hs.5534:AA195173
 R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525.96//Hs.70589:
 25 AA868470
 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223.60//Hs.162:X16302
 R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434.98//
 Hs.25664:AF089814
 30 R-NT2RP2005683//ESTs//1.5e-98:494.96//Hs.22595:AA394229
 R-NT2RP2005690//ESTs//4.8e-43:286.86//Hs.150727:AI292236
 R-NT2RP2005694//EST//3.1e-82:386.100//Hs.149391:AI273643
 R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos taurus]//2.8e-68:376.93//Hs.
 9095:AA532630
 35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503.98//Hs.61638:
 AB018342
 R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500.98//
 Hs.14298:AI417523
 R-NT2RP2005722//EST//6.5e-76:395.94//Hs.142150:AA223982
 40 R-NT2RP2005723//ESTs//1.5e-84:452.93//Hs.91753:RA44255
 R-NT2RP2005726//ESTs//3.5e-64:500.82//Hs.100526:AI223153
 R-NT2RP2005741//ESTs//4.7e-60:333.93//Hs.107242:R40258
 R-NT2RP2005748//ESTs//3.4e-102:498.97//Hs.82660:N78064
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223.96//
 45 Hs.159651:AF068868
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494.98//Hs.
 26285:AF082516
 R-NT2RP2005763//ESTs//1.1e-97:456.99//Hs.65412:AI362163
 R-NT2RP2005767//ESTs//8.0e-38:204.98//Hs.18460:AA193463
 50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-
 112:559.96//Hs.14214:AI189379
 R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544.96//Hs.
 22151:AI214321
 R-NT2RP2005781//ESTs//1.7e-43:217.99//Hs.144391:AA365664
 55 R-NT2RP2005784//EST//0.0071:217.60//Hs.117332:AA699724
 R-NT2RP2005804//ESTs//8.8e-107:512.98//Hs.15496:W44398
 R-NT2RP2005812//ESTs//9.0e-76:359.99//Hs.113937:AI298746
 R-NT2RP2005815//ESTs//5.5e-76:363.99//Hs.136230:AA594981

R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.88613:N25122
 R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
 R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062
 R-NT2RP2005857//ESTS//1.0e-115:576:96//Hs.30663:AI338462
 5 R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
 R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
 R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268
 R-NT2RP2005903//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:
 10 94//Hs.16667:T92427
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
 R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419
 R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988
 R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
 15 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II
 [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631
 R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
 R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714
 20 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
 R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26880:N56918
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//
 Hs.46440:U21943
 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
 25 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258
 R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:
 AB014554
 30 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276
 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398
 R-NT2RP2006219//H.sapiens mRNA for DGCRC6 protein//1.2e-94:532:90//Hs.153910:X96484
 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312
 R-NT2RP2006238//ESTs, Highly similar to rAB8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253
 35 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928
 R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262
 R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:
 40 N78664
 R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771
 R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412
 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321
 R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411
 45 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:
 77//Hs.1361:M55053
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.
 115325:D84488
 R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092
 50 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146
 R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63598
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266
 R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478
 R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679
 55 R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947
 R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474
 R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886
 R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

R-nnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829
 R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]/4.1e-109:542:
 97//Hs.7889:AI337112
 R-NT2RP300002//ESTs//1.3e-08:399:59//Hs.126044:AI301598
 5 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:
 AJ011972
 R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219
 R-NT2RP3000047//EST//9.1:130:66//Hs.140208:AA702213
 R-NT2RP3000052//ESTs, Weakly similar to putative p150 [H.sapiens]/3.1e-41:249:90//Hs.156155:AI222202
 10 R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095
 R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574
 R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029
 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715
 R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241
 15 R-NT2RP3000134//EST//4.7e-108:497:99//Hs.125531:AA884000
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:
 AB011164
 R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418
 R-NT2RP3000186
 20 R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882
 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091
 R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306
 R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817
 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819
 25 R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239
 R-NT2RP3000251
 R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]/2.0e-108:532:97//Hs.111086:AI379177
 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073
 R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446
 30 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]/3.6e-103:516:96//Hs.4894:
 AI191323
 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117
 R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438
 R-NT2RP3000324
 35 R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267
 R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689
 R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225
 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]/3.1e-110:556:96//Hs.111086:AI379177
 R-NT2RP3000359//EST//4.9e-81:340:92//Hs.126495:AA913741
 40 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]/4.8e-91:439:
 97//Hs.31334:AI144423
 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303
 R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:
 45 AF071185
 R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA6682947
 R-NT2RP3000433
 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
 R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
 50 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102
 R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.
 114963:L34408
 R-NT2RP3000484//Heparin cofactor III//0.98: 166:62//Hs.1478: M58600
 55 R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141
 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667
 R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151
 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161

R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]/0.95:85.71//Hs.5184:AA709151
 R-NT2RP3000542//ESTs/2.6e-53:375.84//Hs.44158:N30180
 R-NT2RP3000561//EST/1.1e-13:170.75//Hs.149421:AI198036
 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071
 5 R-NT2RP3000578//ESTs/2.6e-68:324.100//Hs.5445:AA779447
 R-NT2RP3000582//ESTs/2.1e-25:131:80//Hs.152465:AA563785
 R-NT2RP3000584//ESTs/1.8e-97:460.99//Hs.120698:AI241511
 R-NT2RP3000590//ESTs/2.0e-97:453.100//Hs.105355:AA953817
 R-NT2RP3000592//ESTs/2.8e-91:432.99//Hs.144304:AI190916
 10 R-nnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312
 R-NT2RP3000599//ESTs/3.8e-93:437.99//Hs.23971:AA829880
 R-NT2RP3000605//ESTs/4.2e-111:554.96//Hs.40780:AA422049
 R-NT2RP3000622//ESTs/2.0e-100:473.99//Hs.11387:AI1227394
 R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545.98//Hs.4857:AI090739
 15 R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397.80//Hs.15519:AB018315
 R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:
 99//Hs.152517:AA719022
 R-NT2RP3000644//ESTs//1.0e-44:306.84//Hs.155498:W27084
 20 R-NT2RP3000661//ESTs/3.1e-95:470.97//Hs.126069:W76185
 R-NT2RP3000665//ESTs/3.3e-95:503.94//Hs.34313:W81185
 R-NT2RP3000685//ESTs/2.7e-99:515.94//Hs.9711:R60873
 R-NT2RP3000690//ESTs/3.3e-88:414.99//Hs.1465 89:AI085578
 R-NT2RP3000736
 25 R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-
 ESTERASE DELTA [Rattus norvegicus]/1.8e-07:114.75//Hs.136065:W21960
 R-NT2RP3000753//ESTs/3.1e-99:461.100//Hs.150901:AI10447
 R-NT2RP3000759//ESTs/2.0e-74:384.95//Hs.104222:AA207243
 R-NT2RP3000815//ESTs//8.5e-97:455.99//Hs.158897:AI378583
 30 R-NT2RP3000825//EST//0.0089:343.59//Hs.42897:N20810
 R-NT2RP3000826//EST/3.4e-33:342.74//Hs.162236:AA551582
 R-NT2RP3000836//ESTs/8.8e-24:181.84//Hs.134464:AI151081
 R-NT2RP3000841//ESTs//4.5e-93:491.93//Hs.23618:H98082
 R-NT2RP3000845//ESTs/2.4e-88:473.93//Hs.8312:AA813022
 35 R-NT2RP3000847//ESTs/9.3e-89:460.95//Hs.154106:AI051657
 R-NT2RP3000850
 R-NT2RP3000852//Fibrillin 2//0.55:237.63//Hs.79432:U03272
 R-NT2RP3000859//ESTs/1.4e-96:509.94//Hs.7187:AA576895
 R-NT2RP3000865//EST/4.8e-23:461.66//Hs.162088:AA505741
 40 R-NT2RP3000868//ESTs/5.4e-78:430.93//Hs.102796:N70837
 R-NT2RP3000869//ESTs/8.5e-77:397.94//Hs.84484:AI014673
 R-NT2RP3000875//Mevalonate kinase//3.8e-78:531.84//Hs.75138:M88468
 R-NT2RP3000901//ESTs//2.1e-95:466.97//Hs.10647:AA428217
 R-NT2RP3000904//ESTs/1.6e-79:380.99//Hs.100850:AA479385
 45 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:
 AA035728
 R-NT2RP3000919
 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375.71//Hs.2953:X84407
 R-NT2RP3000980//ESTs/3.3e-72:364.96//Hs.9536:AA114178
 50 R-NT2RP3000994//ESTs/3.5e 111:537.97//Hs.21146:AA683542
 R-NT2RP3001004//ESTs/9.6e-91:456.96//Hs.58974:W87405
 R-NT2RP3001007//ESTs/6.7e-99:482.97//Hs.117737:AI088029
 R-NT2RP3001055//ESTs//0.0012:294.60//Hs.66479:AA863044
 R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486.99//Hs.
 55 145956:AA007349
 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)/0.0012:447:58//Hs.2133:U18991
 R-NT2RP3001084//ESTs/4.3e-102:528.96//Hs.25277:W87874
 R-NT2RP3001096//ESTS//1.1e-110:540.96//Hs.42824:AA873182

- R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832
 R-nnnnnnnnnn/DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325
 R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:
 C06063
- 5 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575
 R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878
 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779
 R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180
 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166
- 10 R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188
 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305
 R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]
 //9.6e-113:552:97//Hs.23900:U82984
- 15 R-NT2RP3001150//ESTs//2.9e-90:444:98//Hs.99601:AA760717
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266
 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460
 R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139
 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963
- 20 R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196
 R-NT2RP3001232//ESTs//1.5e-101:58:94//Hs.21630:AA778399
 R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
 R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:
 AA524416
- 25 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631
 R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997
 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135
 R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857
 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965
- 30 R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651
 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332
 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691
 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571
 R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98999
- 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:
 U35234
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:
 AB007920
- R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653
- 40 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798
 R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090
 R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778
 R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90/
 Hs.96200:AA218942
- 45 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375
 R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232
 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628
 R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186
 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898
- 50 R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158
 R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692
 R-nnnnnnnnnn/Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397
 R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374
- 55 R-NT2RP3001447//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//5.1e-
 101:492:98//Hs.124135:AA910560
 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994
 R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

- R-NT2RP3001457//ESTs/1.5e-52:256:99/Hs.117982:AA644658
 R-NT2RP3001459//ESTs/3.4e-62:299:99/Hs.146098:AA167280
 R-NT2RP3001472//ESTs/4.8e-108:540:96/Hs.69594:N37009
 R-NT2RP3001490//ESTs/3.5e-91:549:88/Hs.6606:AA211783
 5 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds/1.4e-61:338:93/Hs.519:U13395
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds/6.8e-112:549:97:Hs.28285:AF064801
 R-NT2RP3001527//ESTs/4.4e-105:543:95/Hs.158761:AA631047
 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds/7.9e-59:427:83/Hs.5247:AF029750
 10 R-NT2RP3001538//ESTs/1.1e-94:521:92/Hs.6846:AA209463
 R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]/2.8e-76:392:95/Hs.66048:
 AA524416
 R-NT2RP3001580//ESTs/3.7e-82:398:98/Hs.23490:N49477
 R-NT2RP3001587//Homo sapiens mRNA for HRIIFB2115, partial cds/1.8e-09:86:88/Hs.4311:AB015337
 15 R-NT2RP3001589//ESTs/0.0029:243:62/Hs.158924:AA605194
 R-NT2RP3001607//EST/0.00096:76:78/Hs.140319:AA748328
 R-NT2RP3001608//ESTs/3.8e-105:525:96/Hs.144655:AI279798
 R-NT2RP3001621//ESTs/3.3e-108:535:97/Hs.47378:AI193598
 R-NT2RP3001629
 20 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds/2.7e-109:541:96/Hs.9899:AF099149
 R-NT2RP3001642//ESTs/6.0e-105:525:96/Hs.3376:AA915989
 R-NT2RP3001646//ESTs/4.8e-95:523:92/Hs.64036:AA127709
 R-NT2RP3001671//ESTs/0.0013:367:60/Hs.106090:AA457030
 R-NT2RP3001672//ESTs/3.4e-37:191:98/Hs.57475:AI382189
 25 R-NT2RP3001676//ESTs/1.5e-81:408:97/Hs.142547:N67648
 R-NT2RP3001678//ESTs/4.3e-85:405:99/Hs.121915:AI268225
 R-NT2RP3001679//ESTs/3.4e-100:545:93/Hs.5943:AI222558
 R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds/8.6e-46:301:87/Hs.40100:AB002390
 R-NT2RP3001690//ESTs/3.3e-111:542:97/Hs.86149:AI341312
 30 R-NT2RP3001708//ESTs/1.4e-96:349:95/Hs.17975:AA868618
 R-NT2RP3001712//ESTs/9.3e-14:102:92/Hs.78041:N29669
 R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
 //4.1e-80:444:91/Hs.6823:W18181
 R-NT2RP3001724//ESTs/1.1e-109:547:96/Hs.14570:AI422099
 35 R-NT2RP3001730//ESTs/4.1e-98:528:92/Hs.155115:AA669923
 R-NT2RP3001739//ESTs/4.4e-87:444:94/Hs.27239:W27810
 R-NT2RP3001752//ESTS/6.1e-93:490:94/Hs.4210:AA740440
 R-NT2RP3001753//ESTs/2.5e-82:395:99/Hs.126435:AA912968
 R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]/1.2e-87:450:96/Hs.20281:
 40 N92517
 R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]/1.1e-21:119:99/Hs.44268:AA455900
 R-NT2RP3001799//OX40L RECEPTOR PRECURSOR/2.8e-45:374:79/Hs.129780:X75962
 R-NT2RP3001819//ESTs/2.6e-87:432:96/Hs.10414:AI291292
 R-NT2RP3001844//ESTs/0.024:128:67/Hs.25131:N50117
 R-NT2RP3001854//ESTs/1.4e-92:490:92/Hs.15165:N52900
 R-NT2RP3001855//ESTs/1.1e-66:361:93/Hs.10043:D81792
 50 R-NT2RP3001896//ESTs/1.4e-96:343:97/Hs.24809:N73642
 R-NT2RP3001898//ESTs/4.1e-90:515:91/Hs.4867:AA521180
 R-NT2RP3001915//ESTs/4.4e-32:175:95/Hs.24641:AA954666
 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]/1.0e-40:202:100/Hs.24709:
 AI123300
 55 R-NT2RP3001929//ESTs/6.6e-84:449:94/Hs.26962:AA682781
 R-NT2RP3001931//ESTs/1.1e-41:214:99/Hs.32360:AA534737
 R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
 //1.3e-95:483:96/Hs.5771:W74591

R-NT2RP3001943//ESTs/1.2e-23:169.88//Hs.103930:AA160990
 R-NT2RP3001944//ESTs/2.0e-90:439.97//Hs.103380:AI291325
 R-NT2RP3001969//ESTs/0.95:133.65//Hs.131669:AI025889
 R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310.99//Hs.11449:AI201540
 5 R-NT2RP3002002//ESTs/2.1e-95:562.89//Hs.5997:AA970888
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335.82//Hs.75087:X86779
 R-NT2RP3002007//ESTs/0.12:184.66//Hs.94030:AA846729
 R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291.89//Hs.155464:AF088219
 R-NT2RP3002033
 10 R-NT2RP3002045//ESTs//1.0e-92:555.88//Hs.106411:W29081
 R-NT2RP3002054//EST/0.45:155.63//Hs.5656:D20426
 R-NT2RP3002056//ESTs/1.4e.95:504.93//Hs.17428:AI365221
 R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127.66//Hs.90438:D63486
 R-NT2RP3002062
 15 R-nnnnnnnnnnnn//ESTs/2.1e-113:552.97//Hs.9591:AA069657
 R-NT2RP3002081//ESTs/5.5e-43:212.100//Hs.124852:AA969139
 R-NT2RP3002097//EST/2.3e-10:80.91//Hs.102717:N59148
 R-NT2RP3002102
 R-NT2RP3002108
 20 R-NT2RP3002146//ESTs//5.5e-58:296.97//Hs.65328:AA625385
 R-NT2RP3002147//EST/2.5e-53:387.81//Hs.147928:M249703
 R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534.96//Hs.59523:AA602837
 R-NT2RP3002163//ESTs//2.7e-106:520.97//Hs.21258:AA412293
 25 R-NT2RP3002165//ESTs//7.4e-93:479.95//Hs.27299:AI074024
 R-NT2RP3002166//ESTs/1.0:281.59//Hs.132817:AA593713
 R-NT2RP3002173//ESTs//2.7e-93:512.92//Hs.23648:H07120
 R-NT2RP3002181//ESTs/1.0e-84:435.96//Hs.47378:AI193598
 R-NT2RP3002244//ESTs//2.7e-11:97.89//Hs.9412:W72446
 30 R-NT2RP3002248//ESTs//4.3e-90:459.95//Hs.9848:AA130588
 R-NT2RP3002255//ESTs/1.3e-45:289.88//Hs.9100:AA431672
 R-NT2RP3002273//ESTs//2.3e-100:489.97//Hs.8258:AA744743
 R-NT2RP3002276//ESTs//1.2e-50:306.91//Hs.16160:AA778171
 R-NT2RP3002303//ESTs/1.1e-67:323.99//Hs.129761:AA836898
 35 R-NT2RP3002304//ESTs//2.8e-86:405.99//Hs.29643:AA418500
 R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]//1.8e-19:136.87//Hs.106928:AI041737
 R-NT2RP3002343//ESTs/1.0e-42:260.93//Hs.7797:W25667
 R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221.64//Hs.556:L41887
 40 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516.94//Hs.6483:Y16355
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524.95//Hs.12707:AB014578
 R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108.71//Hs.28914:Y00486
 45 R-NT2RP3002501//ESTs/2.7e-96:489.95//Hs.27335:N7795
 R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526.90//Hs.8083:AA521436
 R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497.98//Hs.6650:AA843246
 50 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438.94//Hs.19542:AB018272
 R-NT2RP3002549//ESTs//3.8e-98:493.96//Hs.7358:AA191673
 R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184.63//Hs.89230:AF031815
 R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138.78//Hs.129883:AB007880
 55 R-NT2RP3002590//ESTs//2.9e-95:51.290.93//Hs.162942:AI243850
 R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58.100//Hs.76691:AF070673
 R-NT2RP3002603
 R-NT2RP3002631//ESTs//4.8e-54:367.85//Hs.13109:AA192514

R-NT2RP3002659//ESTs//5.3e-30 229 85//Hs.152114:AA401385
 R-NT2RP3002660//ESTs//1.9e-88 452 95//Hs.120146:AA708573
 R-NT2RP3002663//EST//3.2e-89 469 95//Hs.105767:AA525172
 R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109 537:
 5 97//Hs.19348:AA151678
 R-NT2RP3002682//ESTs//2.3e-98 541 91//Hs.75844:AA115502
 R-NT2RP3002687//ESTs//5.5e-103 498 97//Hs.72728:AA910871
 R-NT2RP3002688//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-101:
 524.95/Hs.32580:AI123601
 10 R-NT2RP3002701//EST//0.87 131 63//Hs.161916:AA483169
 R-NT2RP3002713//ESTs//4.7e-106 542 95//Hs.14479:AA160945
 R-NT2RP3002763//ESTs//1.3e-54 290 94//Hs.142031:AA809159
 R-NT2RP3002770//ESTs//0.047 275 61//Hs.122984:AA526973
 R-NT2RP3002785//ESTs//2.4e-52 255 99//Hs.132959:AI376958
 15 R-NT2RP3002799//EST//8.2e-61 321 94//Hs.140992:R71377
 R-NT2RP3002810//EST//0.19 116 68//Hs.121810:AA775240
 R-NT2RP3002818//ESTs//1.3e-109 531 98//Hs.58924:AI348080
 R-NT2RP3002861//ESTs//2.5e-84 429 95//Hs.23920:AA909678
 R-NT2RP3002869//EST//0.00011.116.71//Hs.161606:AA019641
 20 R-NT2RP3002876//ESTs//0.0024.182.63//Hs.117306:AA687262
 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
 8.1e-14;146.72//Hs.129727:AF035587
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314
 R-NT2RP3002911//ESTs//3.6e-92:436.99//Hs.143917:AI206286
 25 R-NT2RP3002948//EST//1.0 102.65//Hs.144730:AI191975
 R-NT2RP3002953//ESTs//1.8e-107.513.98//Hs.119693:AI201698
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563.56//Hs.127338:
 AB007961
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID-COA LIGASE 1 [Saccharomyces cere-
 30 visiae]//112.0e-56:387.86//Hs.144597:W20143
 R-NT2RP3002972//ESTs//1.7e-97.502.96//Hs.7274:AA476850
 R-NT2RP3002978//ESTs//8.6e-104.498.98//Hs.118923:AA252116
 R-NT2RP3002988//EST//1.2e-59.315.94//Hs.157743:AI360533
 R-NT2RP3003008//ESTs//1.4e-97.515.94//Hs.6544:AA524423
 35 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//
 3.0e-100:528.94//Hs.90353:N98551
 R-NT2RP3003059//ESTs//1.7e-76.398.95//Hs.102971:W05355
 R-NT2RP3003061//ESTs//4.9e-82.414.96//Hs.99603:AI141912
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans]//5.9e-83:392.99//Hs.101364:AA534439
 40 R-NT2RP3003071//ESTs//6.3e-85.399.99//Hs.109755:AA180809
 R-NT2RP3003078//ESTs//1.0e-98.471.99//Hs.7795:AI359461
 R-NT2RP3003101//EST//0.032.235.60//Hs.147920:AI202441
 R-NT2RP3003121//ESTs//3.0e-47.238.97//Hs.43559:AI003520
 R-NT2RP3003133//EST//1.5e-77.395.96//Hs.142150:AA223982
 45 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535.96//Hs.
 27437:AA004208
 R-NT2RP3003139//ESTs//2.5e-106.504.98//Hs.106795:AI271632
 R-NT2RP3003150//ESTs//1.6e-99.539.91//Hs.46500:AA129774
 R-NT2RP3003157//ESTs//1.5e-114.563.97//Hs.58608:AA081007
 50 R-NT2RP3003185//ESTs//3.9e-93.443.98//Hs.9741:AI131220
 R-NT2RP3003193//ESTs//2.0e-37.428.71//Hs.33354:AA179944
 R-NT2RP3003197//ESTs//5.8e-56.312.94//Hs.7016:AA215796
 R-NT2RP3003203//EST//0.0073.212.63//Hs.161355:AI422634
 R-NT2RP3003204//ESTs//7.4e-52.253.99//Hs.120146:AA708573
 55 R-NT2RP3003212//ESTs//1.8e-76.401.95//Hs.29067:N26107
 R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229.93//Hs.17377:
 AI078151
 R-NT2RP3003242//ESTs//8.3e-97.458.99//Hs.23057:AI290343

- R-NT2RP3003251//ESTs/1.5e-60:320.95//Hs.36495:AA151628
 R-NT2RP3003264//ESTs/2.1e-103:521.95//Hs.4094:AA173960
 R-NT2RP3003278//ESTs/8.2e-109:536.96//Hs.23788:AA524061
 R-NT2RP3003282//*Homo sapiens* dynamin (DNM) mRNA, complete cds/2.4e-102:550.93//Hs.11702:L36983
 5 R-NT2RP3003290//EST/4.2e-27:372.70//Hs.159131:AI384035
 R-NT2RP3003301//ESTs/4.4e-56:285.97//Hs.95370:AA601055
 R-NT2RP3003302//EST/7.2e-10:395.63//Hs.162554:AA584818
 R-NT2RP3003311//ESTs/4.2e-110:538.97//Hs.62180:AI341261
 R-NT2RP3003313//ESTs/2.1e-106:531.96//Hs.22630:C05931
 10 R-NT2RP3003327//ESTs/4.3e-102:518.95//Hs.120355:AA625445
 R-NT2RP3003330//ESTs/8.6e-104:497.97//Hs.72071:AI125289
 R-NT2RP3003344//ESTs/2.5e-105:494.99//Hs.112188:AA872993
 R-NT2RP3003346//ESTs/1.0:123.69//Hs.116029:AA813102
 R-NT2RP3003353//EST/0.0014:162.68//Hs.149191:AI246155
 15 R-NT2RP3003377//EST/4.5e-15:119.85//Hs.148129:AA885567
 R-NT2RP3003384//EST/0.0057:86.74//Hs.127735:AA962272
 R-NT2RP3003385//ESTs/0.64:347.59//Hs.5646:W72721
 R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.e-24:418.67//Hs.139488:AI124095
 20 R-NT2RP3003409//ESTs/5.3e-98:479.97//Hs.155198:AA767372
 R-NT2RP3003411//ESTs/4.8e-86:416.97//Hs.129059:AA126041
 R-NT2RP3003427//ESTs/7.4e-103:510.96//Hs.25303:AA641023
 R-NT2RP3003433//ESTs/3.5e-85:405.99//Hs.63131:AA664156
 R-NT2RP3003464//*Homo sapiens* rab3-CAP regulatory domain mRNA, complete cds/3.6e-97:479.96//Hs.14934:
 25 AF004828
 R-NT2RP3003490//*Homo sapiens* mRNA for KIAA0725 protein, partial cds/4.1e-102:527.93//Hs.26450:
 AB018268
 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549.94//Hs.7886:
 AI057529
 30 R-NT2RP3003500//Human RP3 mRNA, complete cds/0.66:401:60//Hs.75307:U02556
 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n(CGT)n repeat-containing mRNA//4.1e-33:217.88//Hs.
 8068:U00952
 R-NT2RP3003552//ESTs/3.1e-106:546.94//Hs.101754:AI123430
 R-NT2RP3003555//ESTs/3.4e-106:537.95//Hs.85550:AA187681
 35 R-NT2RP3003564
 R-NT2RP3003572//ESTs/1.2e-20:122.88//Hs.8253:N48721
 R-NT2RP3003576//ESTs/2.7e-71:394.94//Hs.151136:R99944
 R-NT2RP3003589//EST/0.58:242.59//Hs.130804:AA894759
 R-NT2RP3003625//ESTs/7.6e-41:349.80//Hs.140608:N53448
 40 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds/0.26:222:60//Hs.17217:U49957
 R-NT2RP3003659//ESTs/2.0e-113:547.97//Hs.23369:AA769310
 R-NT2RP3003665//ESTs/1.6e-80:415.95//Hs.141084:H11714
 R-NT2RP3003672
 R-NT2RP3003686//ESTs/6.8e-114:552.97//Hs.43299:N23036
 45 R-NT2RP3003701//ESTs/2.1e-16:282.66//Hs.115512:AI208768
 R-NT2RP3003716//ESTs/2.1e-45:195.91//Hs.41296:N71923
 R-NT2RP3003726//*Homo sapiens* mRNA for KIAA075 protein, complete cds//5.6e-103:492.97//Hs.48513:
 AB018300
 R-NT2RP3003746//ESTs/1.9e-85:411.98//Hs.54835:AI050863
 50 R-NT2RP3003795//EST/6.2e-97:459.99//Hs.134769:AI089747
 R-NT2RP3003799//ESTs/2.8e-62:337.94//Hs.124023:H18913
 R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551.95//Hs.115742:
 AF077754
 R-NT2RP3003805//ESTs/2.2e-103:490.99//Hs.9412:W72446
 55 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456.95//Hs.5555:
 AI285198
 R-NT2RP3003819//Interleukin 10//3.3e-43:173.89//Hs.2180:M57627
 R-NT2RP3003825//ESTs/1.6e-66:485.80//Hs.7405:W27761

R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]/[9.6e-98:5.11:95//Hs.26955:AI333224
 R-NT2RP3003831//ESTs/[2.2e-38:317.79//Hs.142173:AA757743
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence/[5.2e-110:541:97//Hs.25300:
 AF070611

5 R-NT2RP3003842//EST/[9.9e-44:506:70//Hs.139093:AA166888
 R-NT2RP3003846//ESTs/[4.6e-10:66:100//Hs.74924:AI332962
 R-NT2RP3003870//ESTs/[3.4e-82:449:92//Hs.122691:AA152298
 R-NT2RP3003876//ESTs/[1.9e-89:449:96//Hs.45046:N40170
 R-NT2RP3003914//ESTs/[1.3e-99:470:98//Hs.118966:AA926726

10 R-NT2RP3003918//ESTs/[1.3e-79:417:94//Hs.5005:W25933
 R-NT2RP3003932//ESTs/[6.0e-83:427:94//Hs.93581:H50221
 R-NT2RP3003989//ESTs/[4.8e-76:403:93//Hs.127243:W80409
 R-NT2RP3003992//ESTs/[2.4e-88:508:90//Hs.134200:D19593
 R-NT2RP3 004013//ESTs/[3.7e-111:551:97//Hs.105108:AA781142

15 R-NT2RP3004016//ESTs/[1.7e-81:394:98//Hs.63368:AA613714
 R-NT2RP3004041
 R-NT2RP3004051//ESTs/[3.5e-69:386:93//Hs.51347:T72820
 R-NT2RP3004070//ESTs/[5.5e-10:552:9511Hs.23392:AI310139
 R-NT2RP3004078//ESTs/[3.3e-82:443:93//Hs.26407:W4537

20 R-NT2RP3004093//ESTs/[4.4e-83:426:94//Hs.140932:AI262104
 R-NT2RP3004095//ESTs/[0.00013:93:78//Hs.36567:AA262045
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]/[3.5e-
 76:402:95//Hs.55847:W31092

25 R-NT2RP3004125//ESTs/[9.3e-74:363:97//Hs.32988:C01696
 R-NT2RP3004145//ESTs/[2.6e-96:451:99//Hs.59584:AA587334
 R-NT2RP3004148//ESTs/[1.3e-10:77:92//Hs.135890:AI183425
 R-NT2RP3004155//ESTs/[1.7e-110:558:96//Hs.27003:AI279093
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]/[1.8e-40:
 200:100//Hs.26089:AA195126

30 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]/[1.1e-41:266:89//Hs.6314:AA522619
 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE
 C13A11.04C [Schizosaccharomyces pombe]/[3.7e-112:547:97//Hs.99819:AI346680
 R-NT2RP3004215//ESTs/[1.1e-103:541:95//Hs.124918:N64794
 R-NT2RP3004242//ESTs/[4.5e-105:524:96//Hs.29724:N46252

35 R-NT2RP3004246//EST/[1.9e-07:67:91//Hs.125687:AA884827
 R-NT2RP3004253//EST/[2.9e-88:454:94//Hs.127713:AA961628
 R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]/[1.6e-89:
 468:95//Hs.5117:AA831530

40 R-NT2RP3004262//ESTs/[4.1e-86:443:96//Hs.101393:T87623
 R-NT2RP3004334//EST/[0.00057:206:63//Hs.149388:AI273630
 R-NT2RP3004341//EST/[0.00042:151:68//Hs.148498:AI200264
 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds/[5.9e-61:299:85//Hs.154103:AF061258
 R-NT2RP3004349//EST/[3.6e-42:175:88//Hs.161917:AA483223
 R-NT2RP3004378//ESTs/[0.27:294:60//Hs.66479:AA63044

45 R-NT2RP3004399//ESTs/[5.8e-99:479:98//Hs.120234:AA732224
 R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]/[0.30:253:58//Hs.97184:AA385934
 R-NT2RP3004428//ESTs/[2.8e-48:279.91//Hs.106826:W25985
 R-NT2RP3004451//ESTs/[4.8e-101:509:96//Hs.29725:W74621
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds/[9.3e-108:526:98//Hs.27349:
 50 AB007917

R-NT2RP3004466//ESTs/[0.25:51:90//Hs.7778:AA195616
 R-NT2RP3004470//EST/[0.032:70:71//Hs.147925:AI249332
 R-NT2RP3004472//ESTs/[0.0069:430:59//Hs.116651:AA993406
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds/[5.0e-107:521:97//Hs.5003:AB007925

55 R-NT2RP3004480
 R-NT2RP3004490//ESTs/[4.7e-68:354:95//Hs.163721:H42504
 R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]/[3.4e-100:508:95//Hs.
 47393:AA218858

R-NT2RP3004503//ESTs//4.6e-90:478.93//Hs.133998:AA994735
 R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//1.8e-83:465.92//Hs.137064:AA318257
 R-NT2RP3004507//ESTs//1.5e-98:495.96//Hs.128905:AI051971
 5 R-NT2RP3004527//ESTs//1.6e-109:535.97//Hs.149481:AI279865
 R-nnnnnnnnnnnn
 R-NT2RP3004544//EST//0.035:226.60//Hs.99195:AA449232
 R-NT2RP3004566//ESTs//4.1e-86:455.95//Hs.13110:T67461
 R-NT2RP3004569//ESTs//2.9e-94:493.94//Hs.24948:AA977674
 10 R-NT2RP3004572//ESTs//1.1e-92:437.99//Hs.24846:AI420493
 R-NT2RP3004578//ESTs//0.98:166.64//Hs.124593:AA854456
 R-NT2RP3004594//EST//5.8e-89:426.98//Hs.134213:AI080213
 R-NT2RP3004617//ESTs//1.4e-40:226.85//Hs.15921:R71157
 R-NT2RP3004618//ESTs//1.8e-38:229.90//Hs.125153:AA453723
 15 R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds//7.2e-57:291.95//Hs.8786:AB014680
 R-NT2RP4000008//ESTs//8.9e-119:561.98//Hs.25035:AI123335
 R-NT2RP4000023//EST//1.2e-34:271.80//Hs.98300:AA418560
 R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320.82//Hs.155464:AF088219
 20 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289.82//Hs.51233:AF016266
 R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462.99//Hs.10114:AI345945
 R-NT2RP4000078//ESTs//0.00068:367.60//Hs.106090:AA457030
 R-NT2RP4000102//ESTs//9.7e-50:256.97//Hs.24266:R28287
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536.96//Hs.57929:AB011538
 25 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554.97//Hs.64691:AB007952
 R-NT2RP4000147//ESTs//3.9e-11:122.80//Hs.25584:AA632014
 R-NT2RP4000150//EST//4.4e-84:510.88//Hs.144238:W52294
 R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III
 30 [C.elegans]//5.7e-93:515.92//Hs.8083:AA521436
 R-NT2RP4000159//ESTs//0.0019:209.65//Hs.161816:AA400295
 R-NT2RP4000167//ESTs//2.1e-113:549.97//Hs.109441:N66569
 R-NT2RP4000185//ESTs//0.65:232.59//Hs.144445:AA807257
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505.96//Hs.13999:
 35 AB014600
 R-NT2RP4000212//ESTs//8.5e-14:169.75//Hs.8520:AA081788
 R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272.90//Hs.40100:AB002390
 R-NT2RP4000218//ESTs//6.1e-10:335.64//Hs.105658:AA978185
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP) //2.9e-70:354.96//Hs.155481:
 40 AJ006470
 R-NT2RP4000246//ESTs//7.1e-26:154.94//Hs.14838:AA502757
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379.99//Hs.43728:
 AF091092
 R-NT2RP4000263
 45 R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104:525.96//Hs.152069:AA548972
 R-NT2RP4000312//ESTs//8.2e-66:319.99//Hs.35091:AI271631
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513.99//Hs.13410:AF070524
 R-NT2RP4000323//ESTs//7.7e-109:534.97//Hs.34790:AA192760
 50 R-NT2RP4000356//ESTs//3.1e-44:320.83//Hs.141323:N80390
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520.99//Hs.107479:
 AB018281
 R-NT2RP4000367//Homo sapiens l kappa B kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-
 110:527.98//Hs.31323:AF044195
 55 R-NT2RP4000370//ESTs//8.9e-32:166.98//Hs.70488:AI301130
 R-NT2RP4000376//ESTs//8.8e-99:465.99//Hs.27182:AA604498
 R-NT2RP4000381//ESTs//3.0e-50:280.93//Hs.8395:W27376
 R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:

91/Hs.26156:AA630975
 R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]/[8.9e-95:468:96//Hs.93871:AI191318
 R-NT2RP4000424//ESTs/[3.7e-98:473:98//Hs.24945:AI189011
 5 R-NT2RP4000448//ESTs/[2.6e-99:446:91//Hs.25159:R60955
 R-NT2RP4000449//ESTs/[3.6e-98:468:98//Hs.31176:AI037953
 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds/[0.35:153:63//Hs.113286:U77783
 R-nnnnnnnnnnnn//ESTs/[4.5e-89:455:96//Hs.62638:AA127740
 10 R-NT2RP4000480//ESTs/[4.9e-92:431:99//Hs.121072:AI204167
 R-nnnnnnnnnnnn
 R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [C.elegans]/[1.2e-40:125:97//Hs.56124:AI424792
 R-NT2RP4000515//EST/[6.7e-30:183:90//Hs.150710:AI122713
 15 R-NT2RP4000517//Aldehyde dehydrogenase 7/[7..5e-28:183:76//Hs.83155:U10868
 R-NT2RP4000518//EST/[0.091:178:58//Hs.133031:AI049874
 R-NT2RP4000519
 R-NT2RP4000524//ESTs, Highly similar to rsec8 [R.norvegicus]/[3.4e-93:496:93//Hs.107394:H07126
 R-NT2RP4000528//EST/[8.84:130:66//Hs.140208:AA702213
 20 R-NT2RP4000541//EST/[5.2e-63:337:94//Hs.156337:AI337328
 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]/[8.2e-92:448:98//Hs.25597:H93026
 R-NT2RP4000588//ESTs/[3.8e-94:445:98//Hs.44077:N28840
 R-NT2RP4000614//ESTs/[6.5e-18:159:83//Hs.24549:N57263
 25 R-NT2RP4000638//ESTs/[2.5e-46:296:87//Hs.132722:AA618531
 R-NT2RP4000648//ESTs/[2.6e-103:559:93//Hs.23794:W80393
 R-NT2RP4000657//ESTs/[1.0:189:60//Hs.87073:AA972704
 R-NT2RP4000704//ESTs/[2.8e-101:509:96//Hs.84824:AA935651
 R-NT2RP4000724//ESTs/[1.5e-83:442:94//Hs.142114:AA205615
 30 R-NT2RP4000728//ESTs/[8.04:61:75//Hs.145334:AI251399
 R-NT2RP4000739//ESTs/[8.8e-80:418:94//Hs.42959:N21211
 R-NT2RP4000781//ESTs/[1.4e-79:376:99//Hs.135458:AI081312
 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds/[3.1e-106:550:94//Hs.25132:AB007939
 35 R-NT2RP4000833//ESTs/[5.8e-46:309:85//Hs.163979:AA828834
 R-NT2RP4000837//ESTs/[1.7e-112:539:97//Hs.97718:AI1334028
 R-NT2RP4000855//ESTs/[1.1e-95:486:95//Hs.5345:AA988104
 R-NT2RP4000865//EST/[6.68-412:89//Hs.142196:AA258356
 R-NT2RP4000878//ESTs/[1.9e-80:417:95//Hs.104716:AI023185
 40 R-NT2RP4000879//ESTs/[1.8e-42:211:99//Hs.89991:AI374617
 R-nnnnnnnnnnnn//ESTs/[1.2e-99:453:97//Hs.100182:N92594
 R-nnnnnnnnnnnn//EST/[9.4e-06:197:63//Hs.145970:AI277106
 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]/[5.9e-17:134:85//Hs.14146:W92235
 R-nnnnnnnnnnnn//ESTs/[4.3e-14:84:100//Hs.155360:AA984683
 45 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds/[8.2e-108:548:95//Hs.24812:AF069532
 R-NT2RP4000929//ESTs/[1.3e-119:567:98//Hs.62717:AA044905
 R-NT2RP4000955//ESTs/[3.5e-10:19:78//Hs.42946:N21111
 R-NT2RP4000973//ESTs/[2.8e-05:93:69//Hs.155126:AA563986
 50 R-NT2RP4000975//ESTs/[4.4e-58:324:95//Hs.126070:AA045179
 R-NT2RP4000979//ESTs/[3.5e-42:468:73//Hs.106210:AI193017
 R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence/[8.7e-120:570:98//Hs.12457:AF052123
 R-NT2RP4000989//ESTs/[1.3e-122:581:98//Hs.10499:AA528018
 R-NT2RP4000996//ESTs/[9.2e-113:579:94//Hs.23762:N26620
 55 R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds/[1.1e-28:439:68//Hs.129735:AF010144
 R-NT2RP4001004//ESTs/[3.6e-78:389:98//Hs.156290:AI016769
 R-NT2RP4001006//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]/[6.6e-124:574:99//Hs.

47393:AA218858
R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186.AI418635
R-NT2RP4001029//ESTs//4.4e-11:523:99//Hs.28423.AI336292
R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]/3.6e-114:569:96//Hs.6762:AA088424
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859
R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]/2.1e-103:485:99//Hs.10114:AD45945
R-NT2RP4001078
R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial/1.7e-119:569:98//Hs.
10 106778:AJ010953
R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668
R-nnnnnnnnnnnn/Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164
R-NT2RP4001095//ESTs//1.e-113:563:96//Hs.118732:AI344055
R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314.R999617
15 R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737
R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357
R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476
R-NT2RP4001138//ESTs//3.0e-112:543:97//Hs.57655:AI056890
R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC
20 REGION [Saccharomyces cerevisiae]/5.4e-113:573:96//Hs.5249:U55977
R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453
R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171
R-NT2RP4001150//ESTS//1.9e-90:422:100//Hs.125490:AI138884
R-NT2RP4001159
25 R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555.AA639278
R-nnnnnnnnnnnn//ESTs//1.1e-25:140:97//Hs.83756:AI002822
R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514
R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495
R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]/4.4e-123:624:95//Hs.
30 22744:AI379892
R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750
R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103
R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120
R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255
35 R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430
R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933
R-nnnnnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588
R-NT2RP4001313
R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892
40 R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612
R-NT2RP4001345//ESTs//3.e-89:443:96//Hs.6770:AA972732
R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837
R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616
R-NT2RP4001372
45 R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC
REGION [Saccharomyces cerevisiae]/1.7e-108:546:96//Hs.32271:AA203680
R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299
R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501
R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC
50 REGION [Saccharomyces cerevisiae]/3.8e-79:438:93//Hs.21938:W81045
R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA4743132
R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649
R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [H.sapiens]/1.6e-102:498:97//Hs.62386:AA512948
R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433
55 R-NT2RP4001447
R-NT2RP4001474
R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655
R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846

R-NT2RP4001502//ESTs//6.7e-73:382.96//Hs.11874:N93511
 R-NT2RP4001507//ESTs//2.6e-57:302.96//Hs.65328:AA625385
 R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546.96//Hs.5570:AI377863
 R-NT2RP4001529//ESTs//3.3e-112:524.99//Hs.28423:AI336292
 5 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566.98//Hs.108530:AA523928
 R-nnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:
 88//Hs.136189:AA133224
 R-NT2RP4001555//ESTs//1.1e-95:445.100//Hs.134403:AA677552
 10 R-NT2RP4001567//ESTs//2.8e-106:506.98//Hs.102708:AA292285
 R-NT2RP4001568//ESTs//6.4e-55:300.94//Hs.57442:N63437
 R-NT2RP4001571//ESTs//1.3e-114:556.97//Hs.30340:AA521251
 R-NT2RP4001574//ESTs//0.0035:120.67//Hs.96339:AA225906
 R-NT2RP4001575
 15 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]
 //8.7e-112:557.97//Hs.7558:AA526812
 R-NT2RP4001610//ESTs//6.2e-77:382.96//Hs.21543:AA166776
 R-NT2RP4001614//ESTs//2.8e-117:565.98//Hs.9591:AA089657
 R-NT2RP4001634//ESTs//2.0e-39:213.96//Hs.32360:AA534737
 20 R-NT2RP4001638//Homo_sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559.97//Hs.5332:
 AF007151
 R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192.97//Hs.5662:AA868361
 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II
 [Caenorhabditis elegans]//1.1e-104:525.96//Hs.20472:W28734
 25 R-NT2RP4001677//ESTs//1.8e-106:522.97//Hs.106390:AA156805
 R-NT2RP4001696//Human chromosome 8 BAC clone C19H7SK-2A8 complete sequence//5.7e-118:583.96//Hs.
 15562:U96629
 R-NT2RP4001725//ESTs//2.0e-11:141.74//Hs.117589:N25941
 R-nnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-
 30 CURSOR [D.melanogaster]//3.4e-73:362.97//Hs.152332:AI141922
 R-NT2RP4001739//ESTs//6.6e-59:340.91//Hs.122293:AA843692
 R-NT2RP4001753//Zinc finger protein 3 (A8-51) [5.6e-113:552.96//Hs.2481:X78926
 R-NT2RP4001760//ESTs//2.5e-94:453.98//Hs.122579:AA766315
 R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326.94//Hs.110839:
 35 W28098
 R-NT2RP4001803
 R-NT2RP4001822//ESTs//4.4e-98:526.92//Hs.96908:AI161133
 R-NT2RP4001823//ESTs//1.7e-72:357.97//Hs.144900:AI218434
 R-NT2RP4001828//ESTs//3.3e-101:536.92//Hs.18851:AA857826
 40 R-NT2RP4001838//ESTs//4.2e-58:344.90//Hs.48723:N66663
 R-NT2RP4001849//EST//0.24:105.71//Hs.136747:AA749210
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087
 R-NT2RP4001893//ESTs//3.0e-58:321.95//Hs.158787:W79602
 R-NT2RP4001896//EST//3.8e-15:108.92//Hs.160835:AI345528
 45 R-NT2RP4001901//ESTs//1.2e-110:536.97//Hs.31443:AI018606
 R-NT2RP4001927//ESTs//2.1e-105:546.93//Hs.73291:AI417099
 R-NT2RP4001938//ESTs//2.8e-40:235.78//Hs.163641:R61848
 R-NT2RP4001946//ESTs//1.3e-29:175.93//Hs.43703:AA088436
 R-NT2RP4001950//ESTs//4.6e-95:458.98//Hs.150890:AI341793
 50 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)[2.3e-62:310.82//Hs.73919:X81637
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457.94//Hs.41793:
 AA775879
 R-NT2RP4001975//ESTs//1.9e-52:281.94//Hs.7704:W58252
 R-NT2RP4002018
 55 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:
 90.86//Hs.41127:AA555184
 R-NT2RP4002052//ESTs//0.054:353.60//Hs.117510:AA903738
 R-NT2RP4002058//EST//7.8e-26:151.94//Hs.124617:AA855106

R-NT2RP4002071//ESTs//6.9e-99:475.98//Hs.29216:AA916679
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198
 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507
 5 R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565
 R-NT2RP4002083//ESTs//2.0e-108:548.96//Hs.6120:W60407
 R-NT2RP4002408//ESTs//2.6e-77:391.96//Hs.14014:AA745592
 R-NT2RP4002791//ESTs//7.9e-101:527.93//Hs.22394:N32555
 10 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272
 R-NT2RP4002905//ESTs//1.5e-107:517.98//Hs.40460:N36090
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605.94//Hs.108258:AB007934
 15 R-OVARC1000004
 R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929
 R-OVARC1000013//ESTs//5.9e-98:531.93//Hs.16470:AA121635
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273
 R-OVARC1000017
 20 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286
 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073
 R-OVARC1000060//EST//2.8e-28:348.71//Hs.141728:W73041
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367
 R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R6787
 25 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259
 R-nnnnnnnnnnnn//ESTs//1.0e-111:526.98//Hs.129020:AI380703
 R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596.94//Hs.20597:W58370
 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942
 30 R-OVARC1000106
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495.97//Hs.3688:AF069250
 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489.74//Hs.101238:Y11312
 R-OVARC1000133//EST//0.00028:284.61//Hs.30547:H05482
 35 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214
 R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090
 R-OVARC1000151
 R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023
 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629
 40 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258
 R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864
 R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874
 R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958
 45 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI1223130
 R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079
 R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476
 R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-
 50 37:191:98//Hs.20725:A027777
 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449
 R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743
 R-OVARC1000326//ESTs, Moderately similar to laminin associated polypeptide 1C [R.norvegicus]//1.3e-98:488:
 96//Hs.125749:AI377682
 55 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05923

R-OVARC1000411//ESTs/3.2e-82.395.98//Hs.104747:AA406219
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.e-27.211.79//Hs.108287:L27670
 R-OVARC1000420//EST/2.8e-38.255.74//Hs.138525:R99237
 R-OVARC1000427//EST/2.6e-58.302.96//Hs.122914:AA476734
 5 R-OVARC1000431//ESTs/4.9e-108.551.96//Hs.11668:AI123426
 R-OVARC1000437
 R-OVARC1000440//ESTs/2.9e-91.456.96//Hs.93701:AI018671
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45.320.84//
 Hs.73614:U83460
 10 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79.418.94//Hs.12334:
 AB014583
 R-OVARC1000461//ESTs/3.1e-62.342.93//Hs.23241:R46582
 R-OVARC1000465//ESTs/1.7e-67.349.95//Hs.127238:AA477576
 R-OVARC1000466//ESTs/1.9e-66.337.95//Hs.5212:AI421211
 15 R-OVARC1000473//ESTs/5.4e-89.320.99//Hs.29173:AA134926
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]/1.1e-102.514.96//Hs.11833:AI299947
 R-OVARC1000486//ESTs/3.9e-78.405.95//Hs.98312:AA424983
 R-OVARC1000496
 R-OVARC1000520//ESTs/1.2e-20.145.88//Hs.87456:AA434484
 20 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47.217.87//Hs.155464:AF088219
 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48.264.92//Hs.49860:AA702248
 R-OVARC1000543//ESTs/5.7e-74.410.94//Hs.62817:AA047021
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27.202.85//Hs.90859:X85106
 R-OVARC1000557//EST/2.8e-18.169.79//Hs.149101:AI244285
 25 R-OVARC1000564//EST/2.3e-34.199.92//Hs.146637:AI141587
 R-OVARC1000573//Interleukin 10//4.7e-42.300.83//Hs.2180:M57627
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58.392.84//Hs.155464:AF088219
 R-OVARC1000588//EST/1.8e-41.174.85//Hs.163333:AA879053
 R-OVARC1000605
 30 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47.417.77//Hs.
 158897:AB007970
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28.366.72//Hs.96247:X95073
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31.162.100//Hs.111862:
 AB011162
 35 R-OVARC1000678//EST//0.92:199.60//Hs.122025:AA778480
 R-nnnnnnnnnn//ESTs/0.94-416.59//Hs.130754:AA279522
 R-OVARC1000681//EST//9.2e-21.179.80//Hs.132635:AI032875
 R-OVARC1000689//Homo sapiens ataxin-7 (SCAT7) mRNA, complete cds//0.053:160.64//Hs.108447:AJ000517
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09.141.73//Hs.32511:AB007901
 40 R-OVARC1000703//ESTs/1.7e-46.298.87//Hs.138856:H47461
 R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17.137.86//Hs.7049:
 AI141736
 R-OVARC1000746//ESTs/0.16:366.60//Hs.136969:AA830918
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-
 45 28.430.69//Hs.42457:AA523306
 R-OVARC1000771//ESTs/1.3e-87.461.94//Hs.22399:AA531016
 R-OVARC1000781//ESTs/18.3e-119.572.97//Hs.41972:AA626793
 R-OVARC1000787//ESTs/7.4e-18.115.93//Hs.164036:AA845659
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19.119.95//Hs.3069:L11066
 50 R-OVARC1000802//ESTs/2.2e-41.383.78//Hs.161228:AI419764
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106.536.95//Hs.61628:
 Y17711
 R-OVARC1000846//Clathrin, light polypeptide (Lcb) //1.6e-66.282.87//Hs.73919:X81637
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115.579.96//Hs.18910:AF045584
 55 R-OVARC1000862//EST/4.3e-14.129.81//Hs.150663:AA923096
 R-OVARC1000876//ESTs/1.0e-115.573.96//Hs.87287:AI150674
 R-OVARC1000883//ESTs/3.5e-109.523.98//Hs.28423:AI336292
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

REGION [Bacillus subtilis]/7.9e-98:525:93//Hs.10366:W21953
R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777
R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:II15401
R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350
5 R-OVARC1000912
R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814
R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127
R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696
R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215
10 R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794
R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971
R-OVARC1000959//Small inducible cytokine A5 (RANTES)/(7.2e-44:283:86//Hs.155464:AF088219
R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394
R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909
15 R-OVARC1000984//ESTS, Weakly similar to No definition line found [C.elegans]//3.5e-68:346:96//Hs.25544:
AA532784
R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811
R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874
R-OVARC1001000//ESTs//1.1e-22:198:80//Hs.140608:N53448
20 R-OVARC1001004//Human kpn1 repeatmra (cdna clone pdk-pkn1-4), 3' end//1.7e-28:181:77//Hs.139107:K00629
R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270
R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117
R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630
R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:
25 137.74//Hs.77579:AF013263
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149
R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046
R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384
R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
30 R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231
R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:
AF082657
R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844
35 R-OVARC1001074
R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029
R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,
LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
R-OVARC1001113//Homo sapiens diaphanous 1 (DHD1A) mRNA, complete cds//3.3e-75:386:95//Hs.26584:
40 AF051782
R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.
46468:U45984
R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548
R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312
45 R-OVARC1001161//ESTs, Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! [H.sapiens]//2.2e-
66:346:95//Hs.53263:AA173226
R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223
R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727
R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200
50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)/(1.8e-42:305:84//Hs.155464:AF088219
R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223
R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:
80//Hs.97203:U83171
R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343
55 R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826
R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025
R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668
R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344168
 R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929
 R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708
 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532
 5 R-OVARC1001282//EST/4.0e-51:428:99//Hs.145599:AI263113
 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334.100//Hs.23763:
 AB011090
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)/1.3e-68:304:83//Hs.73919:X81637
 10 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein/1.0:147:63//Hs.76494:U41344
 R-OVARC1001339//Small inducible cytokine A5 (RANTES)/(5.0e-48:452:76//Hs.155464:AF088219
 R-OVARC1001341//ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//6.9e-
 85:464:93//Hs.23651:AA650356
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247
 15 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA4535216
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657
 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844
 R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777
 R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415
 20 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:
 AB011147
 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958
 R-OVARC1001391
 R-nnnnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913
 25 R-OVARC1001417//Homo sapiens EXLIM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651
 R-OVARC1001419
 R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136
 R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427
 R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345
 30 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592
 R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700
 R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694
 R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:
 35 AF016507
 R-OVARC1001506//Small inducible cytokine A5 (RANTES)/(1.8e-48:283:90//Hs.155464:AF088219
 R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492
 R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388
 40 R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7//4.4e-20:150:89//Hs.155160:
 AF031166
 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087
 R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019
 R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965
 45 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869
 R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659
 R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854
 R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080
 R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784
 50 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]/1.2e-27:236:81//Hs.15485:
 AA046954
 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276
 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/(1.7e-62:300:83//Hs.144563:
 AF057280
 55 R-nnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:
 540:92//Hs.117741:AA903456
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//
 1.1e-109:567:94//Hs.155377:U97670

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529.97//Hs.15869:
AB014575

R-OVARC1001768//ESTs//3.5e-59:327.94//Hs.107923:H66127

R-OVARC1001791//ESTs//1.3e-11:565.96//Hs.6107:AA160604
5 R-OVARC1001795//ESTs//2.8e-97:526.93//Hs.72158:AA156978

R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276.81//Hs.153563:AF011333

R-OVARC1001805//ESTs//4.1e-78:375.98//Hs.126902:AT374688

R-OVARC1001812//EST//4.8e-45:349.80//Hs.162677:AA604831

R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519.63//Hs.25639:AB011110
10 R-OVARC1001820//ESTs//9.5e-50:314.80//Hs.140491:W52705

R-OVARC1001828//ESTs//0.11:186.63//Hs.29055:AI374621

R-OVARC1001846//ESTs//0.34:134.66//Hs.152992:AI242161

R-OVARC1001861//ESTs//2.3e-19:120.92//Hs.42225:N31809

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571.91//Hs.25300:
15 AF070611

R-OVARC1001879//EST//1.3e-24:185.85//Hs.136617:AA630476

R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302.90//Hs.153468:
AB011147

R-OVARC1001883//ESTs//1.0e-51:295.93//Hs.164059:AA447310
20 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//
1.6e-87:346.90//Hs.6216:AF061749

R-OVARC1001901//ESTs//6.8e-24:132.98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491.92//Hs.32343:W73855

R-OVARC1001916//ESTs//7.9e-97:491.95//Hs.24989:H7842
25 R-OVARC1001928

R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:
253.88//Hs.117741:AA903456

R-OVARC1001943//ESTs//9.3e-13:78.100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498.94//Hs.
30 22744:AI379892

R-OVARC1001950//EST//1.3e-35:236.81//Hs.132635:AI032875

R-OVARC1001987//ESTs//5.5e-94:514.92//Hs.21148:AI183729

R-OVARC1001989//ESTs//9.7e-46:228.99//Hs.127046:AA935887

R-OVARC1002044//ESTs//3.4e-45:303.85//Hs.132722:AA618531
35 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542.96//Hs.108258:
AB007934

R-OVARC1002066//ESTs//8.5e-97:455.99//Hs.135477:AI088556

R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340.82//Hs.15519:
AB018315

R-OVARC1002107//ESTs//5.9e-103:498.98//Hs.157207:AA629860
40 R-OVARC1002127//ESTs//3.0e-87:419.98//Hs.127833:AI347130

R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME
III [Caenorhabditis elegans]//1.7e-102:485.98//Hs.137516:AA805691

R-OVARC1002143//ESTs//4.2e-92:428.92//Hs.158126:W26825
45 R-OVARC1002156//ESTs//1.6e-38:198.98//Hs.22957:AA478923

R-OVARC1002158//ESTs//7.3e-81:412.96//Hs.12211:AA908631

R-OVARC1002165//ESTs//1.8e-09:154.72//Hs.49354:AA424160

R-OVARC1002182//ESTs//4.3e-80:465.91//Hs.77067:AA040478
50 R-PLACE1000004//ESTs, Weakly similar to TEICOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//
7.5e-32:164.99//Hs.144194:AA706337

R-PLACE1000005//EST//0.37:212.60//Hs.127020:AA934920

R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100.97//Hs.109268:AF070557
55 R-PLACE1000014//EST//9.6e-44:344.77//Hs.161917:AA483223

R-PLACE1000031//ESTs//2.2e-32:374.70//Hs.117969:H94870

R-PLACE1000040//ESTs//0.00017:316.59//Hs.23242:AI310440

R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519.86//Hs.23094:M19503

R-PLACE100005011ESTs//9.7e-90:453.96//Hs.27410:N25612

R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126.97//Hs.1946:L06499

R-PLACE1000066//ESTs, Weakly similar to coded by *C. elegans* cDNA yk10c10.3 [C.elegans]/1.4e-61.331:
 94//Hs.30026;A|356771
 R-PLACE1000078//ESTs//2.6e-30:212.85//Hs.89312:AA167659
 R-PLACE1000081
 5 R-PLACE1000094
 R-PLACE1000133//ESTs//4.4e-87:448.94//Hs.93748:AA884505
 R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]/5.5e-103:538.94//Hs.9670:
 AA632135
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds/4.1e-114:594.94//Hs.
 10 151017:AF058291
 R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]/2.0e-19:114.95//Hs.7036:
 V22072
 R-PLACE1000213//ESTs//9.4e-99:494.96//Hs.24398:AI262946
 R-PLACE1000214//ESTs//5.3e-98:466.98//Hs.28661:AA805916
 15 R-PLACE1000236//Human BENE mRNA, partial cds/1.7e-19:162.84//Hs.85889:U17077
 R-PLACE1000246//EST//0.026:134.86//Hs.135611:Z21545
 R-PLACE1000292//ESTs//2.5e-80:418.96//Hs.138233:N57912
 R-PLACE1000332//EST//1.7e-82:422.96//Hs.118637:T61940
 R-PLACE1000347//ESTs//8.5e-36:180.100//Hs.6377:AA632424
 20 R-PLACE1000374//ESTs//2.8e-90:434.98//Hs.161785:AI423126
 R-PLACE1000380//ESTs//1.0e-81:399.97//Hs.47105:AI334994
 R-PLACE1000383//ESTs//3.7e-75:405.94//Hs.23200:AA203708
 R-PLACE1000401//ESTs//1.4e-16:212.72//Hs.151665:AA020959
 R-PLACE1000406//ESTs//2.1e-51:259.97//Hs.129651:N53089
 25 R-PLACE1000420//ESTs//7.7e-92:471.95//Hs.144407:AA737799
 R-PLACE1000421//ESTs//2.9e-14:282.67//Hs.142068:AA176125
 R-PLACE1000424//EST//2.9e-35:453.70//Hs.162404:AA573131
 R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete
 30 cds//1.6e-47:472.77//Hs.113259:AF023456
 R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [H.sapiens]/2.0e-58:410.81//
 Hs.97579:AA398118
 R-PLACE1000453//ESTs//2.3e-85:442.95//Hs.9725:AA035793
 R-PLACE1000481//ESTs, Weakly similar to Ndr protein kinase [H.sapiens]/3.2e-109:549.95//Hs.19074:U69566
 R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]/3.5e-83:
 35 435.94//Hs.26510:AA700425
 R-PLACE1000504//ESTs//3.2e-58:281.99//Hs.118270:AA844729
 R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208.88//Hs.153026:
 AB014540
 R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC
 40 REGION [Saccharomyces cerevisiae]/1.9e-26:220.81//Hs.163791:W25348
 R-PLACE1000564//ESTs//1.1e-54:302.92//Hs.158520:AI380485
 R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404.75//Hs.153014:AB02353
 R-nnnnnnnnnnnn/Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542.82//Hs.62661:M55542
 R-PLACE1000596//ESTs//0.028:364.59//Hs.106090:AJ357030
 45 R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds/4.3e-49:295.90//Hs.154326:D42087
 R-PLACE1000610//ESTs//0.0010:104.74//Hs.17413:N45301
 R-PLACE1000636//ESTs//1.8e-64:340.95//Hs.100895:AA479308
 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:
 96//Hs.5819:AF102265
 50 R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and
 LLNLc110F1857Q7 (RZPD Berlin))/1.4e-102:559.92//Hs.29595:AJ005896
 R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:
 64//Hs.128763:AF009353
 R-PLACE1000712//ESTs//7.8e-60:317.95//Hs.8245:AA115485
 55 R-PLACE1000716
 R-PLACE1000748//ESTs//8.9e-87:466.93//Hs.25245:AA176701
 R-PLACE1000749//EST//0.019:186.61//Hs.135443:AI077396
 R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H.4.8 IN CHROMOSOME III [C.el-

egans]/[3.9e-40:224.94//Hs.87889-AA262008
R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence/[6.5e-27:531.66//Hs.133342:AF070536
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds/[8.5e-103:513.96//Hs.31921:
AB014548
5 R-PLACE1000786//ESTs/[5.2e-93:449.97//Hs.58389:W74428
R-nnnnnnnnnn/H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219
R-PLACE1000798//ESTs/[1.1e-97:508.94//Hs.139119:N32189
R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]/[7.7e-31:220:86//Hs.
117576:R33135
10 R-nnnnnnnnnn//ESTs/[1.8e-87:459.94//Hs.43100:AA186588
R-PLACE1000856//ESTs/[0.0084:224:59//Hs.145906:AI275039
R-PLACE1000863//ESTs, Highly similar to PLATELET 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces
cerevisiae]/[2.2e-92:467:95//Hs.6118..-AI141558
R-PLACE1000909//ESTs/[4.7e-89:435.97//Hs.95744:AI392846
15 R-PLACE1000931//ESTs/[1.9e-28:261:73//Hs.135545:AI097091
R-PLACE1000948//ESTs/[0.034:329:58//Hs.114851:AA608697
R-PLACE1000972//EST/[3.3e-24:264:74//Hs.130321:AI002941
R-PLACE1000977//EST/[0.085:153:65//Hs.131646:AI025689
R-PLACE1000979
20 R-PLACE1001000//ESTs/[4.7e-56:284.96//Hs.117978:AA810725
R-PLACE1001007//ESTs, Moderately similar to MKN1 [H.sapiens]/[5.2e-63:343:93//Hs.5662:AA868361
R-PLACE1001010//EST/[0.96:53.71//Hs.96973:AA351146
R-PLACE1001015//Oxytocin receptor/[2.8e-25:308:71//Hs.2820:X64878
R-PLACE1001024//ESTs/[5.0e-12:79.96//Hs.97910:AA404736
25 R-PLACE1001036//ESTs/[4.0e-15:301:65//Hs.137947:AI025762
R-PLACE1001062//ESTs/[5.2e-15:199:73//Hs.138982:AA056120
R-PLACE1001076//ESTs/[3.9e-84:406:98//Hs.115455:AA678124
R-PLACE1001088//ESTs/[3.0e-106:518:97//Hs.158964:AA639580
R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds/[0.035:259:59//Hs.31575:AF100141
30 R-PLACE1001104//ESTs/[6.1e-115:582:95//Hs.10972:AA164268
R-PLACE1001118//ESTs/[6.9e-81:440:93//Hs.5383:AA913610
R-PLACE1001136//ESTs/[7.4e-41:168:83//Hs.95115:AA206594
R-PLACE1001168//ESTs/[3.9e-21:116:99//Hs.5897:AA148834
R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]/[0.91:77:71//Hs.
35 11521:AA287527
R-PLACE1001185//ESTs/[1.5e-65:330:96//Hs.26368:AA789297
R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]/[1.9e-99:512:
94//Hs.24884:AA176812
R-PLACE1001241//ESTs/[1.1e-81:446:93//Hs.42278:AI073464
40 R-PLACE1001257//EST/[6.4e-46:298:87//Hs.162404:AA573131
R-PLACE1001272//ESTs/[0.31:158:61//Hs.42960:N95371
R-PLACE1001279//ESTs/[1.8e-77:376:97//Hs.29276:AA427780
R-PLACE1001280//ESTs/[1.1e-30:134:89//Hs.163492:AI334460
R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.mus-
45 culus]/[2.7e-22:181:84//Hs.48320:AA149548
R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]/[4.2e-34:195:92//Hs.86276:
W27601
R-PLACE1001311//ESTs/[9.1e-91:438:97//Hs.41055:AI339056
R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds/[5.5e-44:215:86/
50 Hs.50984:U01160
R-PLACE1001351//ESTs/[2.4e-101:494:97//Hs.23944:AI097077
R-PLACE1001366//Small inducible cytokine A5 (RANTES)/[8.7e-43:284:85//Hs.155464:AF088219
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds/[2.3e-81:431:93//Hs.152005:
AF009615
55 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence/[1.0e-36:192:97//Hs.12342:AF055030
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds/[1.0e-86:
456:94//Hs.21301:AF093419
R-PLACE1001387//ESTs/[6.0e-74:383:94//Hs.55016:AI298280

R-PLACE1001395//ESTs//2.3e-94:473.95//Hs.22394:N32555
 R-PLACE1001399//ESTs//2.6e-41:204.100//Hs.24462:N36348
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242.95//Hs.110404:
 AF091087
 5 R-PLACE1001414//ESTs//0.0013:77.75//Hs.144614:AA291800
 R-PLACE1001440
 R-PLACE1001456//EST//0.76:120.62//Hs.34011:H48115.
 R-PLACE1001468//ESTs//4.0e-80:403.96//Hs.131832:AI017547
 R-PLACE1001484//ESTs//3.0e-16:201.72//Hs.153413:AI248625
 10 R-PLACE1001502//ESTs//8.1e-31:161.99//Hs.126264:AA455617
 R-PLACE1001503//ESTs//2.4e-37:176.81//Hs.141581:AA315361
 R-PLACE1001517//Homo sapiens hGAA mRNA, complete cds//2.1e-57:339.90//Hs.4742:AB006969
 R-PLACE1001534//ESTs//3.6e-61:304.97//Hs.45207:AI042153
 R-PLACE1001545//TESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.6e-22:
 15 170.85//Hs.155456:AA707265
 R-PLACE1001551//ESTs//1.5e-39:202.98//Hs.139269:AA894431
 R-PLACE1001570//EST//1.1e-70:495.82//Hs.144234:W52249
 R-PLACE1001602//EST//0.33:297.57//Hs.149839:AI287601
 R-PLACE1001603//ESTs//2.0e-17:181.76//Hs.155334:AA827904
 20 R-PLACE1001610//EST//1.1e-86:442.95//Hs.112580:AA608683
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217.97//Hs.75258:
 AF054174
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458.91//Hs.
 114547:AA167095
 25 R-PLACE1001634//ESTs//0.0035:40.97//Hs.101577:AI168526
 R-PLACE1001640//ESTs//0.0028:377.57//Hs.131044:D61640
 R-PLACE10016727//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//0.98:
 141.62//Hs.153060:AA195804
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-
 30 113.545.97//Hs.3688:AF069250
 R-PLACE1001692//EST//3.0e-43:430.75//Hs.162975:AA679124
 R-PLACE1001705//ESTs//3.0e-81:418.94//Hs.22646:AI374903
 R-PLACE1001716//EST//0.76:150.62//Hs.128906:AA983667
 R-PLACE1001720//ESTs//2.4e-64:385.90//Hs.60455:AA010993
 35 R-PLACE1001729//ESTs//2.9e-84:418.96//Hs.134740:AA282171
 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206.89//Hs.6366:AA614113
 R-PLACE1001740//EST//6.5e-05:113.68//Hs.139949:AA644266
 R-PLACE1001745//ESTs//3.3e-92:473.95//Hs.104270:AA236479
 R-PLACE1001746//ESTs//8.8e-93:443.98//Hs.112198:AI423937
 40 R-PLACE1001748//Homo sapiens metallopeptidase 1 (MP1) mRNA, complete cds//4.1e-93:540.89//Hs.4812:
 AF061243
 R-PLACE1001756//ESTs//0.17:157.66//Hs.141565:N64662
 R-PLACE1001761
 R-PLACE1001771//ESTs//0.92:165.62//Hs.473.87:N51980
 45 R-PLACE1001781//ESTs//5.7e-84:437.95//Hs.23363:AA081236
 R-PLACE1001799//EST//0.00039:126.65//Hs.123267:AA807352
 R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//
 1.3e-93:463.95//Hs.40820:FO58953
 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328.75//Hs.155464:AF088219
 50 R-PLACE1001845
 R-PLACE1001869//EST//1.0:207.62//Hs.137298:W32868
 R-PLACE1001897//ESTs//2.4e-23:219.80//Hs.7503:H50009
 R-PLACE1001912//ESTs//1.5e-32:162.78//Hs.136810:AA789098
 R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363.97//Hs.17839:
 55 AF099336
 R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130.66//Hs.151406:
 AB014523
 R-PLACE1001983//ESTs//2.8e-66:334.96//Hs.110155:AA007313

R-PLACE1001989//ESTs//1.3e-88:453.95//Hs.132717:AA171941
R-PLACE1002046
R-PLACE1002052//ESTs//1.7e-79:428.94//Hs.6737:N32595
R-PLACE1002066//ESTs//2.8e-82:427.94//Hs.132972:AA543094
5 R-PLACE1002072//ESTs//0.27:108.66//Hs.123163:AA809619
R-PLACE1002073//EST//5.5e-70:369.95//Hs.132339:AI028552
R-PLACE1002090//ESTs//6.3e-73:361.96//Hs.134469:AA731632
R-PLACE1002115//ESTs//4.6e-34:233.88//Hs.163443:R23311
R-PLACE1002119//ESTs//1.2e-88:444.96//Hs.15725:AA521293
10 R-PLACE1002140//ESTs//6.6e-22:118.100//Hs.22793:W91937
R-PLACE1002150//ESTs//4.0e-96:465.98//Hs.7312:AI167614
R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400.76//Hs.162172:AA534189
R-PLACE1002163//ESTs//3.2e-83:428.95//Hs.137011:AI185965
15 R-PLACE1002171//ESTs//5.3e-68:392.90//Hs.62273:AA143745
R-PLACE1002205//ESTs//1.5e-39:211.95//Hs.28338:N48793
R-PLACE1002213//ESTs//5.1e-38:290.83//Hs.146811:AA410788
R-PLACE1002227//EST//1.3e-14:214.72//Hs.46979:N49892
R-PLACE1002256//ESTs//2.4e-100:484.98//Hs.9343:AI004257
20 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501.81//Hs.23094:M19503
R-PLACE1002319//ESTs//1.4e-28:17.892//Hs.7353:AA209308
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501.93//Hs.18277:AB018271
R-PLACE1002395//ESTs//3.6e-25:248.77//Hs.3853:AA034291
R-PLACE1002399//ESTs//3.6e-27:238.78//Hs.13014:W26381
25 R-PLACE1002433//ESTs//4.3e-108:511.98//Hs.98324:AA621959
R-PLACE1002437//EST//1.2e-06:158.61//Hs.159833:T24110
R-PLACE1002438//Sjogren syndrome antigen B (autobantigen La)/(0.93:176.60//Hs.83715:X69804
R-PLACE1002450//ESTs//1.5e-89:432.98//Hs.47371:AA136333
R-PLACE1002465//ESTs//1.6e-92:488.93//Hs.78110:AA741320
30 R-PLACE1002474//Human matrin-2 precursor mRNA, partial cds//4.9e-23:166.85//Hs.19368:U69263
R-PLACE1002477//ESTs//2.5e-62:305.98//Hs.88605:AA421132
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307.91//Hs.17200:AF042273
R-PLACE1002499//ESTs//7.4e-72:373.96//Hs.128221:AA972429
35 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296.83//Hs.5158:AB007869
R-PLACE1002514//ESTs, Weakly similar to !!! ALU SUBFAMILY SB1 WARNING ENTRY !!! [H.sapiens]//6.4e-14:217.69//Hs.152230:AI140609
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582.85//Hs.88756:AB018256
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116.93//Hs.99348:AC004774
40 R-PLACE1002537//ESTs//4.8e-93:440.99//Hs.164005:AA766491
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:
95//Hs.23259:AA532437
R-PLACE1002578//EST//1.9e-40:337.81//Hs.162404:AA573131
R-PLACE1002583//EST//1.2e-07:264.65//Hs.156414:AI339738
45 R-PLACE1002591//ESTs//2.3e-67:372.94//Hs.143046:N73778
R-PLACE1002598//ESTs, Highly similar to PROTEIN H1715 [Haemophilus influenzae]//1.2e-44:226.97//Hs.
7527:AA843208
R-PLACE1002604//ESTs//3.3e-106:532.96//Hs.86828:AA632147
R-PLACE1002625//EST//3.8e-13:173.74//Hs.138597:H77749
50 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1 β)//1.0:189.58//Hs.75703:J04130
R-PLACE1002665//Homo sapiens C cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:
390.97//Hs.124903:AF068180
R-PLACE1002714//ESTs//8.2e-63:340.93//Hs.7973:H19830
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445.90//Hs.
55 29202:R71586
R-PLACE1002768//ESTs//1.2e-70:359.95//Hs.132600:H12865
R-PLACE1002772//ESTs//8.1e-49:362.82//Hs.141254:AI334099
R-PLACE1002782//ESTs//2.4e-58:284.98//Hs.143545:AI149014

R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
 5 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.83012:R96142
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
 10 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
 R-PLACE1002962
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
 15 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
 R-PLACE1002993//ESTs, Weakly similar to !!! ALU SUBFAMILY SB WARNING ENTRY !!! [H.sapiens]//1.3e-86:
 502:89//Hs.32232:AA604268
 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268
 R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
 20 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:
 U04840
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.
 25 6318:AI131178
 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
 30 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
 R-PLACE1003176
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802
 35 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//
 Hs.73614:U83460
 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131
 R-PLACE1003258//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//8.3e-102:
 40 551:92//Hs.52431:AA625326
 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.
 29147:AA883993
 R-PLACE1003334//ESTs, Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//3.3e-94:463:
 45 97//Hs.155050:AA908765
 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete
 cds//1.1e-99:469:98//Hs.6564:U92715
 50 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.68748:AB007941
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
 55 R-PLACE1003383//ESTs//0.0084:177:64//Hs.120695:AI377755
 R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

R-PLACE1003478//ESTs//1.0..162:63//Hs.147003:AI184671
 R-PLACE1003493//ESTs//1.2e-73:383.95//Hs.28852:R64270
 R-PLACE1003516//ESTs//3.2e-23:206.80//Hs.138632:H97952
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA/RNA/1..7e-22:236.79//Hs.2853:Z29505
 5 R-PLACE1003521//ESTs//5.8e-74:371.96//Hs.30818:AA194980
 R-PLACE1003528//ESTs//1..1e-40:219.82//Hs.138856:H47461
 R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338.98//Hs.
 110439:N93209
 R-PLACE1003553//ESTs//2.2e-87:438.97//Hs.132022:AI040321
 10 R-PLACE1003566//ESTs//1.2e-62:298.92//Hs.30799:AI052591
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145.80//Hs.
 92381:AB007956
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264.65//Hs.158253:
 R86178
 15 R-PLACE1003584
 R-PLACE1003592//ESTs//1.3e-15:213.69//Hs.139507:T77542
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459.89//Hs.23884:AD77106
 R-PLACE1003596//ESTs//0.011:273.61//Hs.17179:AA142875
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576.88//Hs.56851:D83200
 20 R-PLACE1003605//ESTs//3.7e-86:407.99//Hs.136057:AA988299
 R-nnnnnnnnnnnn//ESTs//1.0..78:71//Hs.101248:T26466
 R-PLACE1003618//ESTs//6.8e-30:281.79//Hs.114455:AA11943
 R-PLACE1003625//ESTs//7.2e-78:377.98//Hs.102708:AA292285
 R-PLACE1003638//ESTs//6..7e-38:274.82//Hs.138852:AA284247
 25 R-PLACE1003669//ESTs//9.7e-83:418.95//Hs.4842:AI342607
 R-PLACE1003704//ESTs//3.0e-13:99.89//Hs.81648:W26521
 R-PLACE1003709//ESTs//0.019:178.60//Hs.32100:N59866
 R-PLACE1003711//ESTs//0.99:126.63//Hs.47005:N98639
 R-PLACE1003723//ESTs//1..7e-89:448.96//Hs.157222:AA766987
 30 R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087
 R-PLACE1003760//Human globin gene/L9e-98:538.91//Hs.100090:ME69023
 R-PLACE1003762//EST//2.9e-15:125.85//Hs.162083:AA497512
 R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965
 R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798
 35 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757
 R-PLACE1003784//ESTs//3.7e-87:428.97//Hs.157985:AI366909
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236.88//Hs.153468:
 AB011147
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-
 40 62:313:96//Hs.121020:AA526092
 R-PLACE1003850//ESTs//4.0e-67:351.96//Hs.159303:T91059
 R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058
 R-nnnnnnnnnnnn
 R-PLACE1003870//EST//2.9e-34:281.79//Hs.160895:AI365871
 45 R-nnnnnnnnnnnn
 R-PLACE1003886//ESTs//6.7e-85:410.97//Hs.25129:W93595
 R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915
 R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282.96//Hs.58553:
 50 AA100804
 R-PLACE1003915//EST//0.87:55.76//Hs.145930:AI275760
 R-PLACE1003923//ESTs//1.7e-89:456.95//Hs.14125:AA156236
 R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110
 R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567
 55 R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330
 R-PLACE1004104//ESTs//1.9e-46:254.94//Hs.96802:AA443231
 R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052
 R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

R-PLACE1004128//ESTs//5.3e-80:415.95//Hs.11835:AA040244
 R-PLACE1004149//ESTs//7.2e-25:331.72//Hs.141084:H11714
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491.76//Hs.113283:AF018080
 R-PLACE1004161//ESTs//2.0e-59:355.88//Hs.13830:AA918601
 5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//
 4.7e-78:434.91//Hs.153504:AF044321
 R-PLACE1004197
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//
 1.5e-105:501.98//Hs.24640:AF069493
 10 R-PLACE1004242//ESTs//1.0e-71:364.87//Hs.138632:H97952
 R-PLACE1004256//EST//0.0011:347.61//Hs.131385:AI022630
 R-PLACE1004257//EST//0.027:99.71//Hs.97587:AA398209
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124
 R-PLACE1004270//ESTs//0.011:264.59//Hs.110044:AA181800
 15 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:
 121:66//Hs.1938:S82362
 R-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds//1.4e-107:581:
 91//Hs.127007:AF084830
 R-PLACE1004284//ESTs//5.0e-22:187.82//Hs.23141:W92114
 20 R-PLACE1004289//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//2.9e-28:
 279:77//Hs.38687:AA744496
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313.95//Hs.
 71435:A1253099
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588
 25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:
 77//Hs.1361:MM5053
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:
 379:93//Hs.16232:AF100153
 R-PLACE1004376//ESTs//0.49:362.59//Hs.138086:AI056309
 30 R-PLACE1004384//EST//1.047:76//Hs.128546:AA905556
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-
 98:572:90//Hs.14202:N46000
 R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467
 R-PLACE1004425//ESTs//2.7e-85:442.95//Hs.12544:N53665
 35 R-PLACE1004428//ESTs//1.0e-07:114.78//Hs.140225:AA704101
 R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
 encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283
 R-PLACE1004451
 R-PLACE1004460//ESTs//5.4e-14:338.64//Hs.97464:AA662980
 40 R-PLACE1004467//ESTs//3.3e-85:467.92//Hs.9527:W52721
 R-PLACE1004471//ESTs//3.0e-73:389.94//Hs.23240:R46578
 R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194
 R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:
 278.61//Hs.89663:L13286
 45 R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117
 R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493
 R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164
 R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553
 R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332.72//Hs.
 50 115325:084488
 R-PLACE1004550
 R-PLACE1004564//ESTs//5.5e-76:367.98//Hs.49683:AA564742
 R-PLACE1004629//ESTs, Weakly similar to OS-9 precursors [H.sapiens]//8.1e-40:272.87//Hs.7100:W07181
 R-PLACE1004645//ESTs//8.3e-14:83:100//Hs.17270:AA701903
 55 R-PLACE1004646//ESTs//3.7e-22:231.76//Hs.141250:N29734
 R-PLACE1004658//ESTs//2.0e-12:109.84//Hs.23508:AA101113
 R-nnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257
 R-PLACE1004672//ESTs//2.0e-50:256.98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:5.10:91//Hs.
80019:AF035606
R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482
R-PLACE1004686
5 R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374
R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]/3.4e-80:413:94//Hs.23528:
AI279571
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997
10 R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619
R-nnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367
15 R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0806 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.e-
20 108:358:99//Hs.3688:AF069250
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356
R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.
73821:M35663
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185
25 R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901
R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]
//6.5e-71:381:93//Hs.8383:AA013272
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308
30 R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete
cds//1.8e-37:330:78//Hs.113259:AF023456
R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881
R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597
R-nnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI221563
35 R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI24948
R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.
17839:AF09936
R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980
R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]/6.4e-80:409:95//Hs.31945:AA702166
40 R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013
R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106
R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789
R-PLACE1004982//ESTs//1.0e-88:471:98//Hs.106496:AI291776
R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335
45 R-PLACE1005026
R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegi-
cus]//0.72:145:66//Hs.11215:N56719
R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:
AB011147
50 R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase
[C.elegans]/1.2e-106:54:95//Hs.18625:AI074605
R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103
R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985
R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF108080
55 R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end cdcs/8.0e-99:531:92//Hs.75437:L40401
R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336
R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

U91985
R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356-AA493225
R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093-AA203423
R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896-AA777349
5 R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838-AA089013
R-nnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119-AA454227
R-PLACE1005181//ESTs//0.012:172:66//Hs.147107-AA190589
R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577-AA022830
R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792-H45211
10 R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552-R99532
R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310-R16767
R-PLACE1005261//ESTs//0.19:175:62//Hs.124337-AA829524
R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146-AA699633
R-PLACE1005277//ESTs//1.15e-29:314:72//Hs.163710-AA024516
15 R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282-AA970322
R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855-AA197937
R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239-AA215797
R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368-AA206614
R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309-AB007960
20 R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291-AA189343
R-PLACE1005335//ESTs,, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202-AA732975
R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394
R-PLACE1005409//EST//0.43:174:59//Hs.162077-AA479978
25 R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306-AA555304
R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257-AA188423
R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503
R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
R-PLACE1005480//EST//0.99:39:82//Hs.157275-AA1364046
30 R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635-AA032875
R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:
AF071185
R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304-AA443325
35 R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP) //8.9e-20:321:69//Hs.155481:
AJ006470
R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380-AA291325
R-PLACE1005550//ESTs,, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III
[Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927
40 R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288-AA203555
R-PLACE1005557//ESTs,, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR
[Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:WB1261
R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771-R99835
R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050-AA724612
45 R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079-AA276023
R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357-AA026927
R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941-AA261857
R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382-AA808964
R-PLACE1005630
50 R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975-W72452
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:
AF083255
R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054-AA528169
R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
55 3.3e-24:401:66//Hs.129727-AF035587
R-PLACE1005689//ESTs//0.00013:82:79//Hs.116331-AA629355
R-PLACE1005727//EST//0.15:206:63//Hs.105002-AA449332
R-PLACE1005730//EST//0.0014:129:70//Hs.127931-AA969259

R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]/|/1.3e-42:236:94//Hs.23889:A1341137
R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087
5 R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]/|/7.7e-15:88:98//Hs.109857:AA088385
R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941
R-PLACE1005803//ESTs//2.6e-75:41:92//Hs.71414:AA13127
R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693
10 R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058
R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)/|/0.040:435:58//Hs.75770:L41870
R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:A050965
R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471
R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305
15 R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793
20 R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382:70//Hs.23094:M19503
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]/|/1.1e-70:377:93//Hs.5662:AA868361
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729
25 R-PLACE1005953
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]/|/2.2e-83:494:88//Hs.108117:AI097079
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239
R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897
30 R-PLACE1005990
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]/|/3.1e-112:593:93//Hs.11449:AI192946
R-PLACE1006011//ESTs, Moderately similar to NAD(*) ADENYLYLTRANSFERASE [D.melanogaster]/|/5.7e-
35 100:596:88//Hs.24284:AA595596
R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276
R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]/|/4.1e-102:491:98//Hs.61164:AI096332
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765
R-PLACE1006076//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]/|/2.0e-
40 26:213:77//Hs.139007:H74314
R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]/|/2.6e-99:560:91//Hs.5249:U55977
45 R-PLACE1006143//Amyl-1-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)/|/0.038:463:59//Hs.904:U84010
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128
50 R-PLACE1006167//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433
R-nnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]/|/2.7e-79:393:96//Hs.19121:
A125280
R-PLACE1006167//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433
R-PLACE1006195//ESTS, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]/|/6.8e-94:
55 532:91//Hs.105216:AI361807
R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507
R-PLACE1005205//EST//1.7e-89:448:96//Hs.116665:AA669114
R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664

R-PLACE1006225//ESTs//7.2e-96.474.97//Hs.91165:AI079555
R-PLACE1006236//ESTs//8.8e-105.535.95//Hs.7919:AI341472
R-nnnnnnnnnn/Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99.497.95//Hs.3781:AC004142
R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104.532.95//Hs.
5 41151:A1031961
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97.499.95//Hs.31921:AB014548
R-PLACE1006262//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//1.6e-
07.321.62//Hs.53057:W67839
R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100.605.88//Hs.2060:L06132
10 R-PLACE1006318//ESTs//2.4e-102.536.94//Hs.8109:AA005265
R-PLACE1006325//ESTs//5.2e-105.518.96//Hs.102319:AI246503
R-PLACE1006335//ESTs//5.1e-45.254.93//Hs.153585:R70900
R-PLACE1006357//EST//5.e-09.309.62//Hs.132493:AA923168
R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097.381.58//Hs.154797:D42044
15 R-PLACE1006368//ESTs//7.9e-85.412.97//Hs.150587:AI079284
R-PLACE1006371//ESTs//7.7e-74.442.88//Hs.143671:W61053
R-PLACE1006382
R-PLACE1006385//ESTs//5.3e-06.346.61//Hs.163707:AA515748
R-PLACE1006412//EST//7.7e-46.306.86//Hs.149580:AI281881
20 R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43.551.69//Hs.154103:AF061258
R-PLACE1006438//ESTs//1.1e-77.284.86//Hs.24545:AI278629
R-PLACE1006445//ESTs//4.4e-53.259.99//Hs.24481:AA573139
R-PLACE1006469//ESTs//9.4e-102.482.98//Hs.7218:AA936961
R-PLACE1006470//ESTs//1.0.271.57//Hs.144515:AA938297
25 R-PLACE1006482//ESTs//4.0e-61.354.92//Hs.51305:T47418
R-PLACE1006492//EST//1.8e-09.48.91//Hs.144451:AA827722
R-PLACE1006506//ESTs//0.012.161.61//Hs.145333:AI251374
R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15.415.63//Hs.48824:D87717
R-PLACE1006531//ESTs//5.6e-31.213.87//Hs.125153:AA453723
30 R-PLACE1006534//ESTs//6.5e-101.512.95//Hs.27763:W46368
R-PLACE1006540//ESTs//7.3e-40.320.79//Hs.121659:W02522
R-PLACE1006552//EST//0.38.418.56//Hs.140470:AA765214
R-PLACE1006598//ESTs//4.0e-80.409.95//Hs.142868:AI128443
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//
35 9.3e-118.590.95//Hs.155377:U97670
R-PLACE1006617//ESTs//8.1e-31.246.83//Hs.139128:AA205322
R-PLACE1006626//ESTs//0.90.98.68//Hs.96322:AA541615
R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33.315.78//Hs.101359:AB002384
R-PLACE1006640//ESTs//3.7e-26.137.100//Hs.32672:W16522
40 R-PLACE1006673//Interleukin 10//8.4e-47.330.83//Hs.2180:M57627
R-PLACE1006678//ESTs//1.1e-13.87.98//Hs.34035:D87736
R-PLACE1006704//ESTs//2.6e-65.394.89//Hs.30582:D12214
R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102.486.98//Hs.12472:AF038172
R-PLACE1006754//EST//1.0e-61.381.89//Hs.14727:T83861
45 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73.394.93//Hs.7252:AF070622
R-PLACE1006779//ESTs//1.4e-69.405.90//Hs.136235:AA262658
R-PLACE1006782//EST//1.8e-25.197.86//Hs.137257:N33234
R-PLACE1006792//ESTs//1.8e-43.317.84//Hs.139190:N55515
R-PLACE1006795//ESTs//6.4e-68.350.95//Hs.11092:AA916335
50 R-PLACE1006800//ESTs//1.9e-55.268.100//Hs.126695:AA917989
R-PLACE1006805//ESTs//6.6e-91.484.93//Hs.94262:AA768347
R-PLACE1006815//ESTs//2.1e-49.364.83//Hs.142031:AA809159
R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
1.0e-87.481.92//Hs.141263:H64113
55 R-PLACE1006829//ESTs//5.7e-43.332.83//Hs.19906:AA456933
R-PLACE1006860//ESTs//0.96.138.63//Hs.136649:AA-82359
R-PLACE1006867//ESTs//1.4e-98.478.97//Hs.10299:N35008
R-PLACE1006878//EST//8.4e-48.243.97//Hs.54970:N93536

R-PLACE1006883//ESTs/3.1e-46:300:88//Hs.162404:AA573131
 R-nnnnnnnnnnnn//ESTs/3.0e-95:496:94//Hs.47546:AA181348
 R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
 R-PLACE1006917//Endothelin receptor type B/0.00012:451:60//Hs.82002:D13168
 5 R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514
 R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
 R-nnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds/3.2e-25:494:63//Hs.36927:D86956
 R-PLACE1006961//Tyrosine aminotransferase/2.5e-46:471:74//Hs.2999:X52520
 R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]/9.0e-29:324:68//Hs.154257:AI275982
 10 R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636
 R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
 R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
 R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971
 R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503
 15 R-PLACE1007053//ESTs//4.2e-55:550:88//Hs.7984:AI202575
 R-PLACE1007097//ESTs//6.7e-48:493:86//Hs.56406:N1027
 R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202
 R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646
 R-PLACE1007112//ESTs//8.9e-69:371:94//Hs.71922:AA148417
 20 R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948
 R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794
 R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765
 R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998
 R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619
 25 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:
 89//Hs.80598:D50495
 R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909
 30 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023 AI275071
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087
 R-PLACE1007301
 35 R-PLACE1007317
 R-PLACE1007342
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:
 91//Hs.76596:AF096870
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:
 40 488:96//Hs.24359:AA699594
 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877
 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//
 45 Hs.14387:AF093771
 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.
 72165:AI243857
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:
 80//Hs.97203:UB3171
 50 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230
 R-PLACE1007478
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DKS164,
 55 DKS206, DKS230, DKS239, DKS268, DKS269, DKS270, DKS272//0.26:411:60//Hs.79012:M18533
 R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:
 89//Hs.9029:W57657

R-PLACE1007524//ESTs//5.8e-45:297.87//Hs.154923:AA491377
R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422.75//Hs.154326:D42087
R-PLACE1007544//ESTs//8.4e-59:327.93//Hs.27410:N25612
R-PLACE1007547//EST//0.00010:107.71//Hs.146867:AI161404
5 R-PLACE1007557//ESTs//1.6e-43:356.79//Hs.44702:AI148840
R-PLACE1007583//ESTs//1.7e-41:214.97//Hs.155071:AA584257
R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554.93//Hs.21838:AF038179
R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)/0.54:61:65//Hs.76506:J02923
R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537.94//Hs.151046:AF038176
10 R-PLACE1007632
R-PLACE1007645//ESTs//0.99:187.62//Hs.163453:AI344106
R-PLACE1007649//ESTs//2.2e-108:561.94//Hs.24398:AI262946
R-PLACE1007677//ESTs, Moderately similar to !!! ALU SUBFAMILY SB2 WARNING ENTRY !!! [H.sapiens]//
9.0e-37:190.97//Hs.23437:AA707331
15 R-PLACE1007688//ESTs//7.5e-79:409.95//Hs.6166:AI376944
R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]
//3.4e-61:384.89//Hs.92918:AA133274
R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501.88//Hs.
91251:U66685
20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307.59//Hs.54481:D86407
R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374.96//Hs.4812:
AF061243
R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253.88//Hs.
AA476815
25 R-PLACE1007729//ESTs//2.7e-44:392.79//Hs.142375:AA398619
R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556.89//Hs.1513121:
AB014585
R-PLACE1007737//ESTs//1.1e-41:345.80//Hs.114671:N39322
R-PLACE1007743//ESTs//2.8e-17:98.100//Hs.124258:AA976778
30 R-PLACE1007746//ESTs//5.3e-69:413.90//Hs.5297:AA156903
R-PLACE1007791//ESTs, Weakly similar to TEICOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//
8.6e-27:143.98//Hs.144194:AA706337
R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428.76//Hs.23094:M 9503
R-PLACE1007810//ESTs//5.9e-15:143.82//Hs.126257:AI279044
35 R-PLACE1007829//ESTs//2.2e-22:190.84//Hs.142707:W24050
R-PLACE1007843//ESTs//5.3e-110:556.95//Hs.107287:AI308839
R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525.91//Hs.23094:M19503
R-PLACE1007852//ESTs//4.5e-14:174.75//Hs.153419:N52017
R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574.94//Hs.28020:
40 AB018309
R-PLACE1007866//EST//1.8e-48:262.96//Hs.141009:H01178
R-PLACE1007877//ESTs//1.2e-94:478.96//Hs.5999:AI207832
R-PLACE1007897//ESTs//2.3e-92:437.99//Hs.122843:AI189060
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460.95//Hs.
45 92381:AB0007956
R-PLACE1007946//ESTs//2.8e-28:172.78//Hs.126784:AA521510
R-PLACE1007954//ESTs//6.1e-72:366.95//Hs.27842:AI217966
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509.96//Hs.
5671:AF084530
50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:
465.93//Hs.78106:AF079529
R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534.99//Hs.44268:AA455900
R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]
//3.8e-97:493.95//Hs.6141:U69564
55 R-PLACE1008000//ESTs//0.00013:241.65//Hs.44369:AI206835
R-PLACE1008002//ESTs//2.2e-83:397.98//Hs.28780:AI263612
R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]
//2.0e-115:575.95//Hs.92395:AA779854

R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334
 5 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028611
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
 10 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
 R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
 15 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
 R-nnnnnnnnnnnn
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
 20 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHILYLYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//
 Hs.146477:AI128445
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
 25 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-
 41:448:72//Hs.139007:H74314
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:
 30 536:87//Hs.7570:W31010
 R-nnnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
 35 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
 R-PLACE1008437//ESTs//1.1e-54:266:98//Hs.13068:AA001928
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
 40 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
 R-PLACE1008532
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
 45 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI232323
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
 R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:
 AA778649
 R-nnnnnnnnnnnn
 50 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
 R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
 R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612
 R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353
 55 R-PLACE10086507//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.
 147967:AF044333
 R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830
 R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

76/Hs.1361:M55053
R-PLACE1008715//EST//0.63.114.64//Hs.121353:AA758600
R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:
83/Hs.142209:AA73303
5 R-PLACE1008757//ESTs//1.4e-45.226.99//Hs.22822:H06408
R-PLACE1008790//ESTs/0.035.67.76//Hs.153554:AI286313
R-PLACE1008798//ESTs/4.9e-59.285.99//Hs.49018:N79390
R-PLACE1008807//ESTs//1.7e-82.413.96//Hs.130745:AA573217
R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98.499:
95/Hs.7179:AF011905
R-PLACE1008813//ESTs, Weakly similar to coded by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92.490.93//
Hs.110454:H11810
R-PLACE1008851//ESTs//2.4e-84.421.95//Hs.158893:AI378428
R-nnnnnnnnnnnnn
15 R-PLACE1008867//ESTs//1.1e-77.400.95//Hs.44198:AI093502
R-PLACE1008887//Yotocin receptor//1.1e-43.601.67//Hs.2820:X64878
R-PLACE1008902//ESTs/0.023.208.61//Hs.154164:AI246893
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56.344.89//Hs.62318:AB018308
R-PLACE1008925//ESTs//0.17.294.57//Hs.105113:AA457018
20 R-PLACE1008934//ESTs//2.0e-61.339.92//Hs.100448:AA622653
R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//
1.3e-19.488.63//Hs.19570:U66680
R-PLACE1008947//ESTs//1.3e-81.385.99//Hs.71574:AI376573
R-PLACE1009020//ESTs//2.9e-79.419.94//Hs.121816:AA775419
25 R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82.434.94//Hs.34780:AJ003112
R-PLACE1009039//ESTs//2.8e-83.448.92//Hs.129179:AA988520
R-PLACE1009045//ESTs//1.6e-64.318.97//Hs.103423:AA814195
R-PLACE1009048//ESTs//2.7e-17.403.63//Hs.149343:AI249139
30 R-PLACE1009050//ESTs//2.0e-88.475.92//Hs.122925:AA909008
R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME
III [Caenorhabditis elegans]//1.2e-112.555.96//Hs.9663:AA527142
R-PLACE1009090//ESTs//5.0e-13.175.75//Hs.140608:N53448
R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98.161:63//Hs.77608:AL021546
35 R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037.63.84//Hs.39943:AA203136
R-PLACE1009110//ESTs//8.6e-17.307.65//Hs.117264:AA682549
R-PLACE1009111//ESTs//1.9e-57.349.90//Hs.11260:N98983
R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97.501.94//Hs.11123:
AA703945
40 R-PLACE1009150//LAMIN B1//0.064.393.60//Hs.89497:L37747
R-PLACE1009155//TESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36.163.82//Hs.
93332:AA811920
R-PLACE1009158//ESTs//0.30.149.65//Hs.155796:R80005
R-PLACE1009166//ESTs//3.3e-34.292.77//Hs.140255:AA708322
45 R-PLACE1009172//EST//8.9e-21.364.67//Hs.142557:AA464948
R-PLACE1009174//ESTs//2.9e-18.274.70//Hs.139241:AA283707
R-PLACE1009183//ESTs//2.3e-44.297.87//Hs.136839:H93717
R-PLACE10091867//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109.572.94//Hs.54943:
Z78396
50 R-PLACE1009190//ESTs//2.6e-53.318.90//Hs.2525:AA176701
R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33.195.92//Hs.104247:X98248
R-PLACE1009230//ESTs//3.0e-31.153.92//Hs.124116:AA772680
R-PLACE1009246//ESTs//2.7e-90.488.92//Hs.10706:AA809018
R-PLACE1009308//ESTs//0.022.46.97//Hs.36545:AA075423
R-PLACE1009319//ESTs//7.7e-99.533.92//Hs.109654:N91279
55 R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82.578.82//Hs.23094:M19503
R-PLACE1009335//EST//1.3e-64.311.99//Hs.130558:AI004397
R-PLACE1009338//ESTs//6.0e-70.386.93//Hs.3542:AI015782
R-PLACE1009368//ESTs//1.4e-18.107.98//Hs.133303:W04760

R-PLACE1009375//ESTs//8.9e-36:313.76//Hs.24608:AA161260
 R-PLACE1009388//EST//4.4e-11:101.83//Hs.147074:AI188883
 R-PLACE1009398//ESTs//5.7e-63:335.93//Hs.149003:AI243186
 R-nnnnnnnnnnnn//ESTs//3.6e-94:452.98//Hs.103177:W72798
 5 R-PLACE1009410//ESTs//2.2e-112:553.96//Hs.61779:AA195255
 R-PLACE1009434//EST//3.4e-15:109.74//Hs.103742:U48632
 R-PLACE1009443//EST//7.5e-61:302.98//Hs.157787:AI361269
 R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479.90//Hs.76987:AF012872
 R-PLACE1009459//ESTs//9.3e-86:437.95//Hs.104871:AI161427
 10 R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266.89//Hs.155049:
 AC004531
 R-PLACE1009477//ESTs//0.2e-50:367.82//Hs.152788:AA630925
 R-PLACE1009493//ESTs//4.5e-14:150.78//Hs.143918:AA699596
 R-PLACE1009524//ESTs//2.9e-97:454.99//Hs.7189:AA767698
 15 R-PLACE1009539//ESTs//9.1e-94:454.97//Hs.154706:AI262131
 R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:
 289.63//Hs.77579:AF013263
 R-PLACE1009571//ESTs//2.1e-23:125.100//Hs.41767:AA732326
 R-PLACE1009581//ESTs,, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.
 20 sapiens]//0.0012:56.91//Hs.12151:AA001818
 R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547.70//Hs.69157:
 AB014535
 R-PLACE1009596//ESTs//1.9e-102:588.90//Hs.142395:AI374735
 R-PLACE1009607//ESTs//0.0093:107.70//Hs.70932:AA126482
 25 R-PLACE1009613//ESTs//7.5e-101:488.97//Hs.5905:AA946680
 R-PLACE1009621//EST//0.99:261.60//Hs.149030:AI243338
 R-PLACE1009622//ESTs//8.0e-93:508.92//Hs.20967:AI422858
 R-PLACE1009637//EST//8.7e-90:442.97//Hs.121372:AA758701
 R-PLACE1009639//EST//8.5e-49:279.93//Hs.117447:R27213
 30 R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589.92//Hs.21862:
 AB011159
 R-PLACE1009665//ESTs,, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483.79//Hs.140416:
 AA778649
 R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310.97//Hs.109590:AF062534
 35 R-PLACE1009708//ESTs//3.Oe-94:471.96//Hs.40091:N48582
 R-PLACE1009721//ESTs,, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529.92//Hs.3945:AA004210
 R-PLACE1009731//TESTs,, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489.89//Hs.
 26194:AA033989
 R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598.95//Hs.154320:AF046024
 40 R-PLACE1009794//ESTs//7.9e-102:529.95//Hs.42927:N20989
 R-nnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-
 quinone Reductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene
 Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene
 similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.e-
 45 113.549.97//Hs.16411:AL030996
 R-PLACE1009845//ESTs//9.5e-106:560.93//Hs.117751:AI056868
 R-PLACE1009879//ESTs//1.8e-61:399.86//Hs.141012:R68748
 R-PLACE1009886//EST//0.54:153.64//Hs.144281:AA081328
 R-PLACE1009888//ESTs//2.7e-105:520.97//Hs.108646:AA613031
 50 R-nnnnnnnnnn//ESTs,, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594.94//Hs.67466:
 AI219740
 R-PLACE1009921//ESTs//7.6e-05:291.60//Hs.124786:AA825563
 R-PLACE1009924//EST//1.2e-42:216.98//Hs.31742:H20276
 R-PLACE1009925//ESTs//5.4e-30:154.100//Hs.114605:AI043137
 55 R-PLACE1009935//ESTs//1.4e-83:417.97//Hs.131755:AA496543
 R-PLACE1009947//Keratin 9//1.0:273.61//Hs.2783:Z29074
 R-PLACE1009971//ESTs//1.5e-87:424.98//Hs.13781:AI160540
 R-PLACE1009992//ESTs//1.3e-87:531.87//Hs.55044:AA460698

R-PLACE100995//ESTs//1.3e-103:575.91//Hs.71218:C75347
 R-PLACE100997//Small inducible cytokine A5 (RANTES)//1.e-42:286:86//Hs.155464:AF088219
 R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:
 AI141736
 5 R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204
 R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//
 7.6e-104:546.94//Hs.8215:AA521150
 R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905
 R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.
 10 11183AF065482
 R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375
 R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424
 R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA4418615
 R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:
 15 U69567
 R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015
 R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103
 R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270
 R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130
 20 R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359
 R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897
 R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313
 R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466
 R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037
 25 R-PLACE1010231
 R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478
 R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545
 R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04538
 R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788
 30 R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081
 R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568
 R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219
 R-PLACE1010341//EST, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//9.9e-
 32:190:77//Hs.152369:AA504818
 35 R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327
 R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594
 R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:
 AJ224162
 R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152
 40 R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816
 R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:
 AF039081
 R-PLACE1010492
 R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031
 45 R-nnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455
 R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306
 R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033
 R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116
 R-PLACE1010599
 50 R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418
 R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895
 R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475
 R-PLACE1010628//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//6.4e-74:
 391:95//Hs.163495:W57637
 55 R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805
 R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719
 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102
 R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:

91//Hs.22383;R51067
 R-PLACE1010662//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794-AA701659
 R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973
 5 R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//
 Hs.46440:U21943
 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (HCAP-C) mRNA, partial cds//1.2e-56:300:
 95//Hs.50758:AF092564
 R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189
 10 R-PLACE1010743
 R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-
 94:442:96//Hs.3688:AF069250
 R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024
 R-PLACE1010786//ESTs. Highly similar to MYOSIN HEAVY CHAIN 1B [Acanthamoeba castellanii]//7.6e-111:575:
 15 94//Hs.10260:AI126627
 R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558
 R-PLACE1010802//ESTs//0.00021:428:5 8//Hs.70258:AI091203
 R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896
 R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472
 20 R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048
 R-PLACE1010857//ESTs. Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917
 R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090
 R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:
 AB011182
 25 R-PLACE1010891
 R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983
 R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023
 R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)/0.25:190:61//Hs.75716:Y00630
 R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093
 30 R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479
 R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126
 R-nnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:
 AF064244
 R-PLACE1010944
 35 R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519
 R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219
 R-PLACE1010960//ESTs. Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565:
 92//Hs.23259:AA532437
 R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
 40 R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846
 R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867
 R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249
 R-nnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153
 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
 45 R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219
 R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
 R-PLACE1011090//ESTs. Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.6e-54:
 398:84//Hs.108740:W20094
 R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478
 50 R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587
 R-PLACE1011133//ESTs. Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:93//Hs.31257:
 AA875998
 R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
 R-PLACE1011160//Homo sapiens mRNA for HRIFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333
 55 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673
 R-PLACE1011185//ESTs. Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//3.4e-85:442:
 95//Hs.136910:AA810782
 R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

R-PLACE1011219//ESTs/7.6e-98:504:93//Hs.124834:AI138671
 R-PLACE1011221//ESTs/5.2e-23:241:78//Hs.26761:AA203299
 R-PLACE1011229//ESTs/1.9e-90:461:95//Hs.132288:AI027693
 R-PLACE1011263//ESTs/6.6e-56:321:93//Hs.158787:W79602
 5 R-PLACE1011273//ESTs/0.016:131:65//Hs.140466:AA766772
 R-PLACE1011291//ESTs/8.7e-47:267:91//Hs.158806:AI376913
 R-PLACE1011296//ESTs/2.7e-38:225:92//Hs.160934:AI376849
 R-PLACE1011310//ESTs/9.1e-37:196:96//Hs.39326:H71807
 R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291
 10 R-PLACE1011332//ESTs/8.4e-44:217:99//Hs.101365:R60578
 R-PLACE1011340//ESTs, Weakly similar to TEICOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337
 R-PLACE1011375//ESTs/2.2e-35:195:96//Hs.106486:H11376
 R-PLACE1011399//ESTs/0.0096:224:67//Hs.151643:AA001194
 15 R-PLACE1011419//ESTs/4.9e-50:267:95//Hs.7045:AA167337
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102
 R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607
 20 R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887
 R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255
 R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278
 R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294
 25 R-PLACE1011520//ESTs/6.8e-99:477:97//Hs.85077:AA968576
 R-PLACE1011563//ESTs/1.4e-94:514:92//Hs.16471:AA206421
 R-PLACE1011567//ESTs/2.8e-89:417:100//Hs.149770:AI285985
 R-PLACE1011576//Zinc finger protein 91 (HPFT, HTF10)//4.7e-55:267:81//Hs.8597:L11672
 R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548
 30 R-PLACE1011635//ESTs/2.5e-67:332:98//Hs.108194:AA780067
 R-PLACE1011641//ESTs/2.5e-71:J38:100//Hs.153085:AA993965
 R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900
 R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535
 R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036
 35 R-PLACE1011664//Rettin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838
 R-PLACE1011675
 R-PLACE1011682//ESTs/2.4e-90:465:94//Hs.57830:AI312025
 R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503
 40 R-PLACE1011725//ESTs/2.0e-70:340:98//Hs.161725:AA251392
 R-PLACE1011729//ESTs/7.5e-19:180:79//Hs.119516:AA443426
 R-PLACE1011749//Myelin oligodendrocyte glycoprotein (alternative products)//7.3e-40:361:77//Hs.53217:Z48051
 R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627
 45 R-PLACE1011778//ESTs/8.0e-70:372:94//Hs.46765:AA521080
 R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179
 R-PLACE1011858//ESTs/2.6e-69:396:91//Hs.55220:D11563
 R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067
 R-PLACE1011875//ESTs/9.0e-88:420:98//Hs.70897:AA987648
 50 R-PLACE1011891//ESTs/3.9e-17:97:100//Hs.84698:AA725913
 R-PLACE1011896//ESTs/2.8e-23:176:84//Hs.121540:AI275497
 R-PLACE1011922//ESTs/6.6e-35:415:73//Hs.10972:AA164268
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617
 55 R-PLACE1011962//ESTs/3.3e-49:294:90//Hs.106800:AI031969
 R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284:63//Hs.124102:AA701285
 R-PLACE1011982//ESTs/2.9e-51:291:93//Hs.20792:R14890

R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247
R-PLACE1012031//*Homo sapiens* mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:
AB018256
R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069
5 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W85120
R-PLACE2000011//*Homo sapiens* clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:
AF01080
R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211
R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504
10 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868
R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.
154069:U06452
R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013
R-PLACE2000039//*H.sapiens* mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073
15 R-PLACE2000047//*Homo sapiens* class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete
cds//4.1e-45:358:81//Hs.159523:AF001622
R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652
R-PLACE2000061//*Homo sapiens* mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:
AB011147
20 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390
R-PLACE2000072//*Homo sapiens* ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:
AF027219
R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179
R-PLACE2001001//ESTs//8.8e-42:281:86//Hs.150727:AI292236
25 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941
R-PLACE2000111//*Homo sapiens* ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs.
42400:AF022789
R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662
R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988
30 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558
R-PLACE2000140//*Homo sapiens* mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:
AB011134
R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357
R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219
35 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778
R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292
R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067
R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378
R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191
40 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717
R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600
R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363
R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:
AI004779
45 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//
4.8e-68:380:92//Hs.107365:AA720664
R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055
R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380
R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058
50 R-PLACE2000342//*Homo sapiens* ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.
42400:AF022789
R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618
R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848
R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081
55 R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731
R-PLACE2000373//*Homo sapiens* mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277
R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781
R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

R-PLACE2000398//ESTs//4.2e-33.373.74//Hs.155184:AA573189
 R-PLACE2000399
 R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-10:9.540:96//Hs.6762:AA088424
 5 R-PLACE2000411//ESTs//1.6e-89.459:95//Hs.117589:N25941
 R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739
 R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333
 R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEESI42F [C.elegans]//3.0e-113:543:
 97//Hs.16933:AA97602
 10 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523
 R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.30964:AA393986
 R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887
 R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390
 R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714
 15 R-PLACE2000458//ESTs//8.8e-82:473:96//Hs.115897:AA156638
 R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79226
 R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642
 R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13033:AA151838
 R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:
 20 AB011147
 R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763
 R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979
 R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830
 R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727
 25 R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739
 R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792
 R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369
 R-PLACE3000147//ESTs//8.6e-53:310:90//Hs.8230:W07142
 R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815
 30 R-PLACE3000155//ESTs//1.2e-19:192:79//Hs.131350:AA80223
 R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//
 Hs.31532:H18272
 R-PLACE3000157
 R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219
 35 R-PLACE3000160
 R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798
 R-PLACE3000194
 R-PLACE3000197//ESTs//1.4e-3 8:197:88//Hs.146341:AI269930
 R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.
 40 131370:AA927516
 R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476
 R-PLACE3000208//ESTs//1.6e-18:151:82//Hs.155498:W27084
 R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964
 R-PLACE3000220//ESTs//6.4e-40:308:84//Hs.136839:H93717
 45 R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014
 R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878
 R-PLACE3000242//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-
 110:549:95//Hs.13692:AA632002
 50 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307
 R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:
 82//Hs.97203:U83171
 R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782
 R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIP5K) mRNA, com-
 55 plete cds//4.0e-59:45:86//Hs.108966:U48696
 R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830
 R-PLACE3000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627
 R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

114531:N74103
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239.84//Hs.15519:
AB018315
R-PLACE3000339//ESTs//1.3e-109:548.96//Hs.7871:AI041837
5 R-PLACE3000341//EST//1.1e-11:231.68//Hs.131328:AA922688
R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40:291.76//Hs.1721:X58377
R-PLACE3000352//EST//1.8e-72:343.100//Hs.144871:AI202380
R-PLACE3000353//ESTs//2.0e-75:395.95//Hs.107260:W52683
R-PLACE3000362//EST//2.8e-80:381.99//Hs.136233:AA261888
10 R-PLACE3000363
R-PLACE3000365//EST//4.8e-50:307.88//Hs.149580:AI281881
R-PLACE3000373//ESTs//5.8e-60:422.83//Hs.142826:W87430
R-PLACE3000388//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.0e-
35:427.73//Hs.138795:R98534
15 R-PLACE3000399//ESTs//6.5e-05:162.66//Hs.149440:AI274570
R-PLACE3000400//ESTs//8.0e-30:10.63//Hs.17697:AA287528
R-PLACE3000401//ESTs//4.6e-60:326.80//Hs.139555:N48230
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227.62//Hs.142570:AF052160
R-PLACE3000405//Human HsLIM15 mRNA for HsLIM15, complete cds//5.3e-43:315.82//Hs.37181:D64108
20 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302.87//
Hs.73614:U83460
R-PLACE3000413//ESTs//1.6e-116:571.97//Hs.10235:H93077
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300.85//Hs.155464:AF088219
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307.85//Hs.32567:AF073519
25 R-PLACE3000455//ESTs//1.0e-160:64/Hs.156045:AA884461
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440.92//Hs.
153487:U43899
R-PLACE3000477//ESTs//2.4e-113:568.96//Hs.24557:AA142980
R-PLACE4000009//ESTs//1.5e-72:361.96//Hs.10119:A700227
30 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433.95//Hs.105399:
AB018352
R-PLACE4000034//ESTs//7.0e-110:550.96//Hs.76607:AA156240
R-PLACE4000049//EST//0.028:87.75//Hs.89303:AA284031
R-PLACE4000052//ESTs//5.6e-116:553.98//Hs.19067:AA521292
35 R-PLACE4000063//ESTs//5.0e-80:388.98//Hs.135028:AI096444
R-PLACE4000089//ESTs//2.3e-97:479.97//Hs.102425:AA807547
R-PLACE4000093//ESTs//1.5e-82:391.99//Hs.160730:AI142739
R-PLACE4000100
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419.91//Hs.129937:
40 AB007931
R-PLACE4000128//ESTs, Moderately similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//3.8e-
11:184.71//Hs.154278:N45985
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118.100//Hs.
118164:AB007969
45 R-PLACE4000147//EST//1.6e-23:175.79//Hs.162236:AA551582
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306.88//Hs.153468:
AB011147
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:
232.82//Hs.16493:T92186
50 R-PLACE4000222//ESTs//2.2e-53:195.85//Hs.141575:AA211734
R-PLACE4000233//ESTs//2.9e-81:456.93//Hs.124964:R81949
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307.85//Hs.113283:AF018080
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301.83//Hs.155464:AF088219
R-PLACE4000252//EST//1.6e-40:275.85//Hs.162197:AA535216
55 R-PLACE4000261//EST//0.0063:384.58//Hs.136284:AA400442
R-PLACE4000269//ESTs//7.3e-67:345.97//Hs.5000:R44586
R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:
352.77//Hs.77579:AF013263

R-PLACE4000300//EST//0.26.103:68//Hs.144438:AA780782
 R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131
 R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454
 R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460
 5 R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414
 R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478
 R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656
 R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425
 R-PLACE4000387//EST, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//1.9e-
 10 44:379:78//Hs.152369:AA504818
 R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:
 AA778649
 R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502
 R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780
 15 R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:
 AA643063
 R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:
 72//Hs.1361:MM5053
 R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932
 20 R-PLACE4000494//EST&//1.4e-109:525:98//Hs.22539:AI334210
 R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290
 R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527
 R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//
 Hs.23590:U59185
 25 R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532
 R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524
 R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249
 R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889
 R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651
 30 R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438
 R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435
 R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353
 R-THYRO1000107//Interleukin 10//2.8e-43:292:84//Hs.2180:M57627
 R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
 35 1.0e-52:413:80//Hs.140385:AA773359
 R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108
 R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764
 R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:
 AF087142
 40 R-THYRO1000132//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//5.2e-
 49:486:77//Hs.24164:N95217
 R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426
 R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258
 R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.e-
 45 111:554:96//Hs.18894:AA910946
 R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189
 R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.e-41:305:81//Hs.155464:AF088219
 R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219
 R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:
 50 AJ005698
 R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:
 AB014552
 R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063
 R-THYRO1000221//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING
 55 ENTRY !!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349
 R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:
 AB014588
 R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYRO1000253//Sialophorin (gp1.115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075
 R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:NG2925
 R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674
 5 R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068
 R-THYRO1000320//POLYPOXYSTOS LOCUS PROTEIN //I:1.0:321:58//Hs.74648:M73547
 R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175
 R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:
 AB018333
 R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:
 10 U29091
 R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064
 R-nnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250
 R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:
 15 294:84//Hs.151614:AF032456
 R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081
 R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429
 R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601
 R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52368
 R-THYRO1000452//ESTs,, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:
 20 AI309761
 R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426
 R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:
 AB018280
 R-THYRO1000488//Homo sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333
 25 R-THYRO1000501//ESTs//1.5e-46:287:89//Hs.125300:R62360
 R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005
 R-THYRO1000505//ESTs,, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965
 R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511
 R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193
 30 R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:
 AF075587
 R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223
 35 R-THYRO1000605//ESTs,, Weakly similar to monocyticleukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//
 Hs.21907:N24415
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742
 R-THYRO1000637
 R-THYRO1000641//ESTs,, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.
 40 sapiens]//4.9e-46:245:95//Hs.97398:AA398634
 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840
 R-nnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.15573:AA487384
 R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI01063
 45 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713
 R-THYRO1000712
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713
 50 R-THYRO1000756//ESTs,, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-AL-
 PHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624
 R-THYRO1000777
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897
 55 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067

R-THYRO1000829
R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
R-THYRO1000852//ESTs/2.3e-20:157:85//Hs.149580:AI281881
R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
5 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663
R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H097871
R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:
10 566:94//Hs.78106:AF079529
R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.
15 14454:AF047440
R-THYRO1000975//ESTs//9.8e-49:303:89//Hs.149580:AI281881
R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]/1.6e-80:474:93//Hs.106616:A027524
R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777
20 R-THYRO1000988//ESTs//3.5e-42:241:83//Hs.162404:AA573131
R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.
44049:AA521489
R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H093717
R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
25 R-THYRO1001062//ESTs//1.5e-46:291:89//Hs.161917:AA483223
R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
R-THYRO1001100
R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//
6.6e-86:491:89//Hs.89135:AI138834
30 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:
AJ006417
R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N1922
R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853
35 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
R-THYRO1001177
R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151
R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
40 R-THYRO1001262//Human kpn repeat mrna (cdna clone pcd-kpn1-4), 3' end//1.3e-48:349:83//Hs.139107:K00629
R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C/I:0.128:64//Hs.118728:D13640
R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230
45 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.
82314:M31642
R-nnnnnnnnnnnnnn//ESTs//0.16:422:5.9//Hs.23876:AA082935
R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
50 R-THYRO1001365
R-THYRO1001374
R-THYRO001401//Human HsLIM15 mRNA for HsLim15, complete cds//2.5e-48:467:75//Hs.37181:D64108
R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
R-THYRO1001405//ESTs//4.6e-25:197:84//Hs.6907:W72733
55 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197
R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.
159187:AB007977

R-THYRO1001434//ESTs//0.40:161.61//Hs.161993:AA503172
 R-THYRO1001458//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159.66//Hs.104239:AA488082
 R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331.79//Hs.155464:AF088219
 5 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134.76//Hs.15731:AB011135
 R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110
 R-THYRO1001537//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304.80//Hs.108740:W20094
 10 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427.76//Hs.2217:U21936
 R-THYRO1001559//ESTs//0.99:210.62//Hs.33619:AA021594
 R-THYRO1001570//ESTs//4.9e-48:287.91//Hs.27131:AA442413
 R-THYRO1001573//ESTs//2.1e-87:446.95//Hs.143669:AA621958
 15 R-THYRO1001584//ESTs//1.5e-64:354.95//Hs.146222:AA397741
 R-THYRO1001595//ESTs//5.7e-39:366.78//Hs.22562:R54247
 R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288.67//Hs.85112:X57025
 R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359.83//Hs.264:U03886
 R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:dihydroxyacetonephosphate acyltransferase (DHAPAT)
 20 mRNA, complete cds//1.3e-82:434.93//Hs.12482:AJ002190
 R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331.83//Hs.127649:AB007874
 R-THYRO1001656//ESTs//3.8e-19:209.75//Hs.92186:AI080282
 R-THYRO1001661//ESTs//1.4e-56:323.91//Hs.24984:AA534446
 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562.95//
 25 Hs.118633:AJ225089
 R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246.73//Hs.
 67619:AB007957
 R-THYRO1001703//ESTs//1.1e-39:142.97//Hs.110748:AI341726
 R-THYRO1001706//ESTs//2.2e-42:214.99//Hs.112536:AI147691
 30 R-THYRO1001721
 R-nnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147.77//Hs.158196:R53184
 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282.65//Hs.116549:AL009172
 R-THYRO1001746//EST//0.0073:226.61//Hs.146544:AI125323
 R-THYRO1001772//ESTs//2.8e-100:495.97//Hs.144993:AA243474
 35 R-THYRO1001793//ESTs//2.5e-89:430.97//Hs.58127:AA534224
 R-THYRO1001809//ESTs//1.0e-41:327.80//Hs.146811:AA410788
 R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242.83//Hs.
 92381:AB007956
 R-THYRO1001895//ESTs//1.7e-08:213.64//Hs.156056:AI352123
 40 R-THYRO1001907//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314
 R-VESEN1000122
 R-Y79AA1000013//ESTs//0.99:233.57//Hs.132216:AA923289
 R-Y79AA1000033//EST//1.9e-62:324.95//Hs.157692:AI359321
 45 R-Y79AA1000037//ESTs//6.1e-47:234.98//Hs.30773:AA557178
 R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330.89//Hs.153026:
 AB014540
 R-Y79AA1000065//ESTs//2.0e-91:497.94//Hs.37759:H59629
 R-Y79AA1000131//EST//2.3e-16:184.75//Hs.141501:N50792
 50 R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553.95//Hs.23159:
 AA113849
 R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185.62//Hs.79414:D79991
 R-Y79AA1000214//ESTs//1.7e-93:495.94//Hs.11673:W68103
 R-Y79AA1000230//ESTs//3.5e-114:553.98//Hs.47125:AI421812
 55 R-Y79AA1000231//ESTs//1.1e-106:526.97//Hs.82856:AI246624
 R-Y79AA1000258//ESTs//1.5e-99:490.97//Hs.6459:AI092936
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320.84//Hs.84123:AB002363
 R-Y79AA1000313//ESTs//1.7e-105:558.93//Hs.18851:AA857826

R-Y79AA1000328//ESTs//1.9e-76:448.91//Hs.16470:AA121635
 R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210
 R-Y79AA1000346//ESTs//7.9e-12:139.76//Hs.115987:AA483808
 R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//
 5 4.4e-66:339:97//Hs.B215:AA521150
 R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-
 44:279:88//Hs.139007:H74314
 R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018
 R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613
 10 R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758
 R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292
 R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-
 60:362:88//Hs.6381:AI188509
 R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320
 15 R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881
 R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.
 41723:U37426
 R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848
 R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:
 20 AI125280
 R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455
 R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:
 AF060503
 R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC
 25 REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818
 R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:
 95//Hs.83023:AF093670
 R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III
 [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330
 30 R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405
 R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463
 R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433
 R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359
 R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512
 35 R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642
 R-nnnnnnnnnnnn/Carboxypeptidase E//0.018:354:59//Hs.75360:X51405
 R-Y79AA1000805
 R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227
 R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650
 40 R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.
 55836:U85647
 R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079
 R-Y79AA1000968
 R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181
 45 R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049
 R-Y79AA1000985
 R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851
 R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067
 R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407
 50 R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:
 AB011135
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260
 55 R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155
 R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015
 R-Y79AA1001167
 R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884

- R-Y79AA1001185
R-Y79AA1001211//ESTs//1.3e-10:344.97//Hs.49760:AA741051
R-Y79AA1001216//ESTs//5.8e-63:416.88//Hs.8595:W60933
R-Y79AA1001228//ESTs//9.3e-101:483.98//Hs.13916:AI025750
5 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674
R-Y79AA1001236//*Homo sapiens* mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//1.e-110:549.95//Hs.23170:AJ005892
R-Y79AA1001281//ESTs//3.6e-98:466.99//Hs.104442:AA481271
R-Y79AA1001299//*Human Init* mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847
10 R-Y79AA1001312//ESTs//3.4e-92:454.97//Hs.127319:AI191149
R-Y79AA1001323//ESTs//1.6e-67:422.89//Hs.118559:AA870884
R-Y79AA1001384//ESTs//3.1e-104:496.98//Hs.153692:AA604143
R-Y79AA1001391//ESTs//2.2e-77:418.94//Hs.118608:AA101819
R-Y79AA1001394//ESTs//2.1e-78:409.95//Hs.23413:AA579859
15 R-Y79AA1001402//EST//9.3e-08:128.75//Hs.141607:N63891
R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109:553.95//Hs.106616:AI027524
R-Y79AA1001511//ESTs//4.9e-49:271.92//Hs.109045:AA523704
R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260:
20 94//Hs.24884:AA176812
R-nnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563
R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872
R-Y79AA1001555//Collagen, type XI, alpha I//1.0:157:64//Hs.82772:J04177
R-Y79AA1001585//ESTs//1.9e-90:430.98//Hs.48333:AA704508
25 R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237
R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204
R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA897542
R-Y79AA1001647//ESTs//6.8e-92:479.95//Hs.154270:N26486
R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.26252:
30 AA643235
R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//Hs.
108896:R54040
R-nnnnnnnnnnnn
R-Y79AA1001696//ESTs//1.4e-84:478.91//Hs.6606:AA211783
35 R-Y79AA1001705//ESTs//6.7e-107:546.95//Hs.106805:AA418490
R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12. Contains part of a gene for
a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phopholipase C, beta (1-Phos-
phatidylinositol-4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63//
Hs.21864:AL031652
40 R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427:97//Hs.18645:AI023798
R-nnnnnnnnnnnn//ESTs//1.1e-112:558.97//Hs.109755:AA180809
R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530:
91//Hs.72444:W23217
R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582
45 R-Y79AA1001848//*Human adhalin* (DAGC) mRNA, complete cds//0.54:221:58//Hs.99931:L34355
R-Y79AA1001866//ESTs//2.2e-102:498.97//Hs.130683:AI278630
R-Y79AA1001874//ESTs//1.9e-96:377:98//Hs.79707:AA354094
R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652
R-Y79AA1001923//EST//0.19:180.58//Hs.148290:AA908404
50 R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275
R-Y79AA1002083//*Homo sapiens* mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135
R-Y79AA1002089//*Homo sapiens* PYRJN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080
R-Y79AA1002093//*Homo sapiens* GT198 mRNA, complete cds//1.2e-12:80:100//Hs.78185:L38933
R-Y79AA1002103//ESTs//1.3e-52:535.76//Hs.142167:AI417785
55 R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275
R-Y79AA1002125//ESTs//9.8e-68:363.94//Hs.72085:AA193398
R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858
R-Y79AA1002204//ESTs//2.1e-83:434.95//Hs.22979:R43725

R-nnnnnnnnnn//ESTs/1.7e-55:478:76//Hs.154554:AA5552715
 R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.
 50441:AA747428
 R-Y79AA1002210//ESTs/4.2e-16:92:100//Hs.54862:AA248349
 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//
 6.5e-86:518:90//Hs.25682:AA857843
 R-Y79AA1002220//ESTs/1.3e-68:326:100//Hs.131052:AI016274
 R-Y79AA1002229//ESTs/1.9e-98:467:98//Hs.132002:AI039977
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:
 10 AB014592
 R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:
 507:96//Hs.25895:AI341537
 R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
 R-Y79AA1002298//ESTs/0.022:241:62//Hs.118272:N90288
 15 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:
 AB014534
 R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985
 R-Y79AA1002351//ESTs/5.6e-100:489:97//Hs.30318:AA913371
 R-Y79AA1002361
 20 R-Y79AA1002399//ESTs/0.029:149:65//Hs.43872:N26908
 R-Y79AA1002407//ESTs/2.8e-117:552:99//Hs.99519:AI042000
 R-Y79AA1002416//ESTs/2.6e-107:531:96//Hs.6716:AA502753
 R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026
 R-nnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]
 25 //4.4e-62:390:88//Hs.143930:AI207821
 R-Y79AA1002472//ESTs/1.1e-39:234:78//Hs.117969:H94870
 R-Y79AA1002482//ESTs/3.4e-45:312:85//Hs.146811:AA410788
 R-Y79AA1002487//ESTs/1.7e-80:427:94//Hs.49210:N66499

30 Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA100005//DNAJ PROTEIN HOMOLOG MTJ1//1.9E-250//554aa//85%//061712
 C-HEMBA100030
 40 C-HEMBA100046
 C-HEMBA100050
 C-HEMBA100076
 C-HEMBA100156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//
 1.9E-12//368aa//24%//P08553
 45 C-HEMBA100158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G)//5E-16//166aa//36%//P35584
 C-HEMBA100168//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I)//2.9E-14//303aa//25%//P35662
 C-HEMBA100185//RAS-RELATED PROTEIN RAL-A//3.4E-12//125aa//31%//P48555
 C-HEMBA100193
 C-HEMBA100227
 50 C-HEMBA100288
 C-HEMBA100302
 C-HEMBA100304
 C-HEMBA100307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-
 49//107aa//91%//035594
 55 C-HEMBA100369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083)//0//1950bp//98%//
 AL049654
 C-HEMBA1000387
 C-HEMBA1000392

C-HEMBA1000460
C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652
C-HEMBA1000491//RAS-LIKE PROTEIN 2 //2E-22//188aa//31%//P22279
C-HEMBA1000501
5 C-HEMBA1000508
C-HEMBA1000520
C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%//P02826
C-HEMBA1000534
10 C-HEMBA1000555
C-HEMBA1000568
C-HEMBA1000588
C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295
C-HEMBA1000636
15 C-HEMBA1000682
C-HEMBA1000686
C-HEMBA1000719
C-HEMBA1000727
C-HEMBA1000752
20 C-HEMBA1000817
C-HEMBA1000851
C-HEMBA1000867
C-HEMBA1000869
C-HEMBA1000872
25 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//1.6E-30//127aa//40%//P43366
C-HEMBA1000918
C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%//Q19124
30 C-HEMBA1000946
C-HEMBA1000968
C-HEMBA1000971
C-HEMBA1000975
C-HEMBA1001009
35 C-HEMBA1001022
C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.4E-12//131aa//38%//Q01485
C-HEMBA1001052
C-HEMBA1001080
40 C-HEMBA1001085
C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%//P48059
C-HEMBA1001109
C-HEMBA1001122
45 C-HEMBA1001133
C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%//Q06730
C-HEMBA1001140
C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5 //6.8E-79//179aa//80%//P51646
50 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//AB020678
C-HEMBA1001235
C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
C-HEMBA1001281
55 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
C-HEMBA1001303
C-HEMBA1001310

C-HEMBA1001326
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
 5 C-HEMBA1001388
 C-HEMBA1001398
 C-HEMBA1001405
 C-HEMBA1001407
 C-HEMBA1001413
 10 C-HEMBA1001415
 C-HEMBA1001446
 C-HEMBA1001450
 C-HEMBA1001455
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//
 15 63aa//61%//P18850
 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166
 C-HEMBA1001533
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657
 C-HEMBA1001581
 20 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//
 Q63679
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//
 365aa//33%//P33450
 25 C-HEMBA1001702
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//
 99%//AL050386
 C-HEMBA1001731
 C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009
 30 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675
 C-HEMBA1001815
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230
 C-HEMBA1001864
 35 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//
 9.3E-36//395aa//26%//Q63342
 C-HEMBA1001987
 C-HEMBA1002018
 40 C-HEMBA1002049
 C-HEMBA1002084
 C-HEMBA1002125
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//
 P79293
 45 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//
 P43694
 C-HEMBA1002191
 C-HEMBA1002199
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//
 50 P18161
 C-HEMBA1002237
 C-HEMBA1002265
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537
 C-HEMBA1002349
 55 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//
 1847bp//99%//AF092563
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793
 C-HEMBA1002430

C-HEMBA1002439
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74./I/4.2E-24//109aa//55%//Q00994
C-HEMBA1002460
C-HEMBA1002462
5 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//
31%//P17437
C-HEMBA1002477
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1./I/6.8E-53//257aa//36%//P48732
10 C-HEMBA1002515
C-HEMBA1002542
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds./I/6.8E-305//951bp//99%//
AF075587
C-HEMBA1002583
15 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds./I/1.4E-253//1149bp//99%//AB011169
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds./I/0//1539bp//99%//AB018351
C-HEMBA1002688
C-HEMBA1002696
C-HEMBA1002750
20 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds./I/0//1532bp//99%//AB020636
C-HEMBA1002777
C-HEMBA1002794
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds./I/8.2e-314//1437bp//99%//
25 AF071185
C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4./I/2E-304//1383bp//99%//AJ132819
C-HEMBA1002850
C-HEMBA1002863
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEDD8.8 IN CHROMOSOME II./I/1.5E-44//188aa//
30 52%//Q09297
C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds./I/0//1483bp//100%//AB011148
C-HEMBA1002937
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%//
P16157
35 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds./I/0//1752bp//99%//AB020710
C-HEMBA1002954
C-HEMBA1002971
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//
1.2E-27//63aa//100%//P14646
40 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//5 34aa//24%//Q02224
C-HEMBA1003033
C-HEMBA1003035
C-HEMBA1003041
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC
45 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439
C-HEMBA1003067
C-HEMBA1003096
C-HEMBA1003117
C-HEMBA1003129
50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-
1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//
33%//P41940
C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801./I/0//1583bp//99%//
AL079278
55 C-HEMBA1003175
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-
FERASE (EC 2.1.1.61).//5.9E-74//134aa//53%//P44551
C-HEMBA1003199

C-HEMBA1003222
C-HEMBA1003235//TROPOMYOSIN //0.0000023//109aa//33%//Q02088
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-) //7.2E-41//245aa//42%//Q06548
C-HEMBA1003257
5 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR //6E-11//239aa//32%//P32506
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds //5.4E-229//
1043bp//99%//AB024436
C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds //0//791bp//99%//AB011109
C-HEMBA1003322
10 C-HEMBA1003327
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN) //0.00000002//248aa//23%//Q02224
C-HEMBA1003370
C-HEMBA1003380
C-HEMBA1003395
15 C-HEMBA1003402
C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds //0//1732bp//98%//AB020712
C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6e-312//
1414bp//99%//ALK05287
C-HEMBA1003418//TRICHOHYALIN //8.7E-19//281aa//31%//P37709
20 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds //0//511bp//94%//AB013139
C-HEMBA1003447
C-HEMBA1003461
C-HEMBA1003463
C-HEMBA1003528
25 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2) //8.8E-189//360aa//96%//P50480
C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP) //2.1E-68//251aa//52%//P53384
C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-
MA-I) //1.2E-31//71aa//100%//P16874
C-HEMBA1003568//52 KD RO PROTEIN (SJOGEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) //7.9E-
30 49//279aa//32%//P19474
C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1 //6.9E-206//445aa//74%//Q13330
C-HEMBA1003581//ITALIN //4.4E-45//52aa//98%//P26039
C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP) //4.4E-10//118aa//
35%//P19682
35 C-HEMBA1003615
C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds //8.2E-178//501bp//97%//AB015344
C-HEMBA1003621
C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2) //1.2E-75//151aa//99%//Q13207
C-HEMBA1003690//HISTONE DEACETYLASE HDA1 //2.1E-59//249aa//47%//P53973
40 C-HEMBA1003711
C-HEMBA1003807
C-HEMBA1003864
C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT) //3.8E-16//
89aa//46%//P16372
45 C-HEMBA1003959
C-HEMBA1003989
C-HEMBA1004074
C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds //8.5E-221//1188bp//78%//
AF091234
50 C-HEMBA1004146
C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds //0//1893bp//98%//AB023145
C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds //0//1892bp//99%//U50748
C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds //5.7E-217//1217bp//88%//
AF095927
55 C-HEMBA1004246
C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds //4.8E-257//738bp//
99%//AF092094
C-HEMBA1004289

C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds./0//1512bp/96%//AF132955
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds./1.2e-316//1445bp/99%//
 AF089841
 5 C-HEMBA1004596
 C-HEMBA1004693
 C-HEMBA1004736
 C-HEMBA1004753
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds./9.1E-34//515bp/66%//U49082
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds./2.6E-246//1249bp/94%//
 10 L39060
 C-HEMBA1004763
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG./5.4E-11//314aa/58%//P08547
 C-HEMBA1004771
 C-HEMBA1004776
 15 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa/66%//P50851
 C-HEMBA1004806
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa/94%//
 Q00004
 C-HEMBA1004850
 20 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//
 100%//AL080114
 C-HEMBA1004923
 C-HEMBA1004929
 C-HEMBA1004932//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa/100%//Q16401
 25 C-HEMBA1004933
 C-HEMBA1004954
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
 0.00000096//286aa/23%//P12036
 C-HEMBA1005475
 30 C-HEMBA1005581//Homo sapiens SLT2 (SUL2) mRNA, complete cds./0//1721bp/100%//AF133270
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//
 151aa/37%//P16372
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds./3.7E-
 225//1189bp/88%//AF076183
 35 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa/28%//P26043
 C-HEMBA1006377
 C-HEMBA1006467
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa/34%//Q01552
 C-HEMBA1006530
 40 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//
 0.000000043//111aa/40%//Q01485
 C-HEMBA1006795
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa/39%//P16258
 C-HEMBA1006936
 45 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds./1.5E-267//1215bp/99%//
 AP078849
 C-HEMBA1007342
 C-HEMBB1000008
 C-HEMBB1000018
 50 C-HEMBB100024
 C-HEMBB100025
 C-HEMBB100036
 C-HEMBB100037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds./2.8E-187//
 1582bp/80%//AF084928
 55 C-HEMBB100083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa/25%//P11799
 C-HEMBB100103
 C-HEMBB100119//Homo sapiens ASMTL gene./0//1891bp/99%//Y15521

C-HEMBB1000136
C-HEMBB1000215
C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEDD8.5.//
2.7E-12//112aa//47%//Q09530
5 C-HEMBB1000244
C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-
MOSOME V//6.1E-09//242aa//26%//Q23256
C-HEMBB1000338
C-HEMBB1000339
10 C-HEMBB1000391
C-HEMBB1000438
C-HEMBB1000449
C-HEMBB1000589
C-HEMBB1000591
15 C-HEMBB1000623
C-HEMBB1000630
C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//
232aa//28%//P78970
C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671
20 C-HEMBB1000671
C-HEMBB1000673
C-HEMBB1000705
C-HEMBB1000706
C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//
25 U53475
C-HEMBB1000763//Homo sapiens CCG-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase MEKK2 mRNA, complete cds.//
1.2E-126//613bp//97%//AF111105
C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-
30 54//232aa//43%//P39956
C-HEMBB1000807
C-HEMBB1000810
C-HEMBB1000848
C-HEMBB1000852
35 C-HEMBB1000870
C-HEMBB1000887
C-HEMBB1000908
C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102
C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//
40 99%//AF116910
C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974
C-HEMBB1000975
C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-
18//178aa//30%//P28575
45 C-HEMBB1000991
C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//
P51523
C-HEMBB1001014
C-HEMBB1001024
50 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED
NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087
C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.6E-52//331bp//
80%//AF010144
C-HEMBB1001068//Homo sapiens liprin-beta 2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803
55 C-HEMBB1001096
C-HEMBB1001105
C-HEMBB1001117
C-HEMBB1001126

C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds./0//3069bp/99%//AB019435
 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds./4.2E-210//1835bp/76%//AF110267
 C-HEMBB1001153
 5 C-HEMBB1001169
 C-HEMBB1001175//ANKYRIN./6.9E-11//169aa/31%//Q02357
 C-HEMBB1001182
 C-HEMBB1001199
 C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds./0//1816bp/99%//AB023187
 10 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds./1.8E-284//713bp/100%//AF089897
 C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds./1.8E-274//642bp/99%//AF132966
 C-HEMBB1001289
 C-HEMBB1001294//GTP-BINDING PROTEIN TC10./1.2E-79//196aa/80%//P17081
 15 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds./1.3E-129//724bp/86%//J92703
 C-HEMBB1001331
 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa/37%//P98175
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mi-
 20 tochondrial protein, complete cds./1.1E-58//292bp/99%//AF097441
 C-HEMBB1001369
 C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds./0//1586bp/99%//AF100757
 C-HEMBB1001387
 C-MAMMA1002317
 25 C-MAMMA1002319
 C-MAMMA1002385//RIBONUCLEOPROTEIN R897D./0.00000015//206aa/29%//Q02926
 C-NT2RM1000080//UNC-1 PROTEIN./5.9E-25//121aa/31%//Q21190
 C-NT2RM1000242
 C-NT2RM1000257//MAGO NASHI PROTEIN./7.9E-69//143aa/91%//P49028
 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-
 PASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa/97%//P39942
 C-NT2RM1000669
 C-NT2RM1000781
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds./6.3E-172//798bp/99%//AF092138
 35 C-NT2RM1001008
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds./0.00000002//980bp/95%//AF085360
 C-NT2RM1001074
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa/27%//
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudo-
 40 gene similar to MMS2, ESTs and GSSs, complete sequence./0//1740bp/99%//AL031291
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
 POLYMERASE III SUBUNIT 2).//2.2E-144//362aa/71%//P25167
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTER-
 MEDIATE CHAIN).//0.0000043//136aa/31%//P54703
 45 C-NT2RM2000032
 C-NT2RM2000042
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//
 1.3E-36//160aa/40%//P50102
 50 C-NT2RM2000093
 C-NT2RM2000101
 C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds./0//1574bp//
 99%//AF067223
 C-NT2RM2000192
 55 C-NT2RM2000239
 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2e-314//
 1416bp/100%//AL080069
 C-NT2RM2000259

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//3.6E-19//181-aa/34%//
P14918
C-NT2RM2000287
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds./.3.4E-294//863bp/99%//
5 AB020666
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds./.0//1637bp/99%//AB011132
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN//1.8E-14//245aa/29%//P11274
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds./.0//1506bp/99%//
U48251
10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-
OTIDE/1.7E-68//19aa/36%//P50849
C-NT2RM2000374
C-NT2RM2000395
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
15 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT)//1.6E-54//344aa/33%//P32802
C-NT2RM2000407
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73//1E-222//237aa/89%//
Q08469
20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION//0.0000001//
157aa/28%//P36113
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-)//0.0000089//377aa/24%//
P22211
C-NT2RM2000490//SYNAPTOTAGMIN(P65)//1.8E-13//166aa/34%//P41823
25 C-NT2RM2000502
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds./.0//1673bp/99%//AF061243
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//1.3E-12//282aa//
32%//P17437
C-NT2RM2000540
30 C-NT2RM2000567
C-NT2RM2000569
C-NT2RM2000577//ISOEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS)//
1.7E-187//741aa/46%//P73505
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds./.0//3001bp/99%//D86987
35 C-NT2RM2000588//HISTONE DEACETYLASE HDA1//2.8E-60//384aa/40%//P53973
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds./.
0//2712bp/99%//AF156487
C-NT2RM2000599//Homo sapiens F-box protein Lilia (LILINA) mRNA, complete cds./.4.9E-70//838bp/69%//
AF179221
40 C-NT2RM2000624//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPlicing FACTOR
SRP75)//4.4E-32//319aa/35%//Q08170
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds./.0//3791bp/99%//AB018272
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds./.0//2530bp/99%//AB014558
C-NT2RM2000639
45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds./.0//1543bp/99%//AB014576
C-NT2RM2000669
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2)//3.7E-142//285aa/90%//P32391
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1)//3.8E-23//184aa//
36%//Q15404
50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds./.4.4E-23//1065bp/99%//AB015342
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L//5.7E-53//266aa/43%//
P41877
C-NT2RM2000795
C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP)//9.5E-279//545aa//
55 98%//P23514
C-NT2RM2000837
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylose kinase, complete cds./.1.7E-200//927bp/99%//
AB015046

C-NT2RM2000952
 C-NT2RM2000984
 C-NT2RM2001004
 C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809
 5 C-NT2RM2001065
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//
 26%//P46577
 C-NT2RM2001131
 C-NT2RM2001141
 10 C-NT2RM2001152
 C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//
 1335bp//99%//AL080109
 C-NT2RM2001194
 15 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143
 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//
 P48724
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//
 32%//P97924
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-
 20 DOHYDROLASE).//1.3E-180//328aa//99%//P13264
 C-NT2RM2001243
 C-NT2RM2001247
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//
 P53995
 25 C-NT2RM2001291
 C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564l052 (from clone DKFZp564l052).//0//1694bp//99%//
 AL080063
 C-NT2RM2001312
 C-NT2RM2001319
 30 C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584
 C-NT2RM2001345//VEGETABLE INCOMPATIBILITY PROTEIN HET-E1.//0.00000029//334aa//22%//000808
 C-NT2RM2001370
 C-NT2RM2001393
 C-NT2RM2001420
 35 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//
 100%//AL050146
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//
 43aa//57%//P52569
 C-NT2RM2001504
 40 C-NT2RM2001524
 C-NT2RM2001544
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//
 90aa//42%//P38660
 C-NT2RM2001575//52 KD RD PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-
 45 61//312aa//44%//P19474
 C-NT2RM2001582
 C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692
 C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931
 50 C-NT2RM2001930
 C-NT2RM2001935
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//
 212aa//23%//P38250
 55 C-NT2RM2001982
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//
 P37838
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

28%//Q12730
C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME 1//3.1E-12//206aa//
30%//Q09782
C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)//
5 0.00000029//83aa//44%//P40796
C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION//1.1E-89//
425aa//41%//P46837
C-NT2RM2002030//Homo sapiens mRNA for Glutamine-fructose-6-phosphate amidotransferase, complete cds.//
0//1959bp//99%//AB016789
10 C-NT2RM2002049
C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13//0.00000099//338aa//
24%//Q07878
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP)//
5E-62//104aa//57%//Q61990
15 C-NT2RM2002091
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//
1868bp//99%//AF030435
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)//4.9E-13//487aa//
20 26%//P49695
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12//8E-31//105aa//47%//P47805
C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//
99%//AL117402
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
25 POLYMERASE III SUBUNIT 2)//1.1E-155//381aa//72%//P25167
C-NT2RM4000061
C-NT2RM4000104//ZINC FINGER PROTEIN 135//1.5E-81//251aa//53%//P52742
C-NT2RM4000139//R.norvegicus trg mRNA//2.3E-114//1161bp//72%//X68101
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//4.8E-13//686aa//23%//
30 P25386
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10//9.2E-75//439aa//41%//P16381
C-NT2RM4000197
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%//AB018255
C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//
35 633bp//64%//L20303
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//
97%//M99438
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L//0//2030bp//99%//
AJ132637
40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%//AF083246
C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN)/1.5E-21//208aa//35%//Q24371
C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%//AB025412
C-NT2RM4000395
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor//0//1730bp//99%//AJ133769
45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1//8E-20//393aa//
24%//Q10297
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS:
50 BASIC PEPTIDE IB-6, PEPTIDE P-H]//4.8E-11//242aa//31%//P04280
C-NT2RM4000496//SAP1 PROTEIN//8.3E-53//434aa//29%//P39955
C-NT2RM4000511
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)
(FRAGMENT)//1.1E-11//394aa//24%//P16884
C-NT2RM4000520
55 C-NT2RM4000585
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//
1.1E-285//1293bp//99%//AF186273
C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%//AB014587

C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds./0//1652bp/99%//AB020657
 C-NT2RP1000040
 C-NT2RP1000063
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsaf2./0//1162bp/99%//X98834
 5 C-NT2RP1000101
 C-NT2RP1000111//COP1 REGULATORY PROTEIN./4E-116//296aa/51%//P93471
 C-NT2RP1000112
 C-NT2RP1000124
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa/60%//P51859
 10 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds./0//1889bp/98%//AB023165
 C-NT2RP1000170
 C-NT2RP1000191
 C-NT2RP1000202//ANKYRIN./1E-25//302aa/34%//Q02357
 C-NT2RP1000243
 15 C-NT2RP1000259
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds./5.8E-114//616bp//
 93%//AF067730
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, com-
 plete cds./1.3E-275//1249bp/99%//AF053551
 20 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1./8.7E-47//155aa/58%//P32447
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161./1.7E-15//162aa/30%//P25343
 C-NT2RP1000357
 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//
 95%//AL080187
 25 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds./0//1056bp/99%//AB011159
 C-NT2RP1000416
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds./1.8E-94//
 1019bp//63%//AF111423
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-
 30 CRYSTALLIN).//2.4E-10//227aa//25%//Q08257
 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III./2.6E-94//
 254aa//47%//P34580
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa/97%//P09653
 C-NT2RP1000481
 35 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds./0//2728bp/99%//D87686
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-
 27//193aa//35%//P49020
 C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa/94%//
 P97367
 40 C-NT2RP1000581
 C-NT2RP1000630//NECDIN./2.4E-44//227aa//41%//P25233
 C-NT2RP1000688
 C-NT2RP1000695
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds./0//2057bp/99%//E14379
 45 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete
 cds./0//2186bp/99%//AF101434
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-
 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN
 50 ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa/50%//Q07960
 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds./0//1494bp//
 99%//AF067223
 C-NT2RP1000846
 C-NT2RP1000851
 55 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-
 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
 C-NT2RP1000915//AUTOANTIGEN NGP-1./1.7E-19//343aa//25%//Q13823
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds./4.6E-

105/504bp//99-%//U39317
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652
 C-NT2RP1000958//AUTOANTIGEN NGP-1./1.4E-19//343aa//25%//Q13823
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//
 5 M17885
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338
 C-NT2RP1000980
 C-NT2RP1000988
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//
 10 1529bp//61%//L01790
 C-NT2RP1001014
 C-NT2RP1001395
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917
 C-NT2RP1001424
 15 C-NT2RP1001449
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//
 100%//AJ005257
 C-NT2RP1001466
 C-NT2RP1001475
 20 C-NT2RP1001482
 C-NT2RP1001494//MALE STERILITY PROTEIN 2 //7.2E-40//261aa//27%//Q08891
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//
 P42803
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-
 25 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//Q35566
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//
 271aa//89%//P47758
 C-NT2RP1001616
 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594
 30 C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//
 55%//Q34136
 C-NT2RP2000007
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//
 P51523
 35 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//
 34%//Q01730
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//
 0//1390bp//98%//AF061749
 C-NT2RP2000054
 40 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-
 SILON).//9.4E-16//45aa//100%//P49446
 C-NT2RP2000067
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//
 383aa//32%//P33450
 45 C-NT2RP2000079
 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338
 C-NT2RP2000091
 C-NT2RP2000097
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
 50 C-NT2RP2000120
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//
 P41877
 C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
 55 AP47) (GOLGI ADAPTOR AP-147 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
 ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585
 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891
 C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds./.3.4e-315/1430bp//99%//
AB023225
C-NT2RP2000173
C-NT2RP2000175
5 C-NT2RP2000195
C-NT2RP2000205
C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds./.0//2898bp//99%//AB020699
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568
C-NT2RP2000232
10 C-NT2RP2000233
C-NT2RP2000239
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa/33%//P56558
C-NT2RP2000270
15 C-NT2RP2000274
C-NT2RP2000283
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//
25%//Q10297
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676
20 C-NT2RP2000298
C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds./.4.3E-279//
1193bp//99%//UB2381
C-NT2RP2000328
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//
25 226aa//92%//P08760
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116./.6.3E-115//
674aa//46%//P17564
C-NT2RP2000369
C-NT2RP2000412
30 C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//
100%//P52597
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds./.0//1757bp//
99%//AF102265
C-NT2RP2000438
35 C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844
C-NT2RP2000503
C-NT2RP2000510
C-NT2RP2000516
C-NT2RP2000603
40 C-NT2RP2000617
C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds./.0//2482bp//99%//AB014514
C-NT2RP2000656
C-NT2RP2000658
C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
45 C-NT2RP2000704
C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE).//2.7E-100//
488aa//44%//O32038
C-NT2RP2000764//NIFS PROTEIN./.6.6E-36//252aa//42%//P12623
C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds./.0//3347bp//99%//AB020680
50 C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//
29%//Q99104
C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//
P13466
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174
55 C-NT2RP2000819
C-NT2RP2000841
C-NT2RP2000845
C-NT2RP2000863

C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2./0/694aa/99%//060841
 C-NT2RP2000892
 C-NT2RP2000931//MATRIN 3./2.4E-289//467aa/95%//P43244
 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0/2487bp/99%//
 5 AL050390
 C-NT2RP2000938
 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds./0/3458bp/99%//AB018298
 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds./0/1989bp/96%//AB024704
 C-NT2RP2000985
 10 C-NT2RP2001036
 C-NT2RP2001044
 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488./0/2749bp/99%//
 AB007957
 C-NT2RP2001065
 15 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//
 5.8E-46//222aa/45%//Q20939
 C-NT2RP2001081//SYNAPTOTAGMIN IV./4.2E-118//430aa/54%//P50232
 C-NT2RP2001094
 C-NT2RP2001119
 20 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein./0/2514bp/99%//AJ132440
 C-NT2RP2001218
 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMHC).//
 2.2E-10/366aa/28%//P14105
 C-NT2RP2001381
 25 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0/1495bp//
 100%//AL080146
 C-NT2RP2001427
 C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds./0/1748bp/99%//AB018340
 C-NT2RP2001675
 30 C-NT2RP2001721
 C-NT2RP2001907
 C-NT2RP2001969
 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds./4.7E-177//
 1538bp/74%//AF062378
 35 C-NT2RP2002046
 C-NT2RP2002154
 C-NT2RP2002208
 C-NT2RP2002270//AF-9 PROTEIN./0.00000012//74aa/36%//P42568
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein./0/2333bp/99%//Y16521
 40 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds./8.4E-254//1158bp//99%//AB015594
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds./4.3E-240//
 1105bp/99%//AF038958
 C-NT2RP2002426
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds./0/2180bp/99%//
 45 AB005289
 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X./6.2E-19//288aa//26%//
 Q11073
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//
 42%//P12815
 50 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa/38%//
 P55345
 C-NT2RP2002621
 C-NT2RP2002672
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II./1.9E-14//210aa//
 55 30%//O14345
 C-NT2RP2002769
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//
 203aa/27%//P29764

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds./1.9E-138//623bp//100%//AF038392
 C-NT2RP2002954
 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) //4.6E-80//147aa//100%//P51669
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10 //0.0000001//98aa//36%//P10129
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds./0//2209bp//99%//AB026190
 C-NT2RP2003108
 10 C-NT2RP2003117
 C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds./2.3E-82//642bp//68%//AF079765
 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN) //2.4E-38//539aa//25%//P004652
 C-NT2RP2003177
 15 C-NT2RP2003194
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds./0//1580bp//99%//AF151811
 C-NT2RP2003295//Homo sapiens RMP mRNA for RP58 meidating protein, complete cds./0//1526bp//99%//AB006572
 C-NT2RP2003329//PUTATIVE ADENYLYLATE CYCLASE REGULATORY PROTEIN //3.6E-14//332aa//32%//
 20 P26337
 C-NT2RP2003367
 C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT //5E-131//269aa//91%//P38378
 C-NT2RP2003446
 C-NT2RP2003533
 25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-) //1.7E-17//148aa//34%//P74261
 C-NT2RP2003596
 C-NT2RP2003629
 C-NT2RP2003687
 30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //5.4E-29//85aa//72%//Q05481
 C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) //1.7E-75//147aa//93%//P51669
 C-NT2RP2003793
 35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B) //1.5E-23//200aa//30%//O09175
 C-NT2RP2003986
 C-NT2RP2004042
 C-NT2RP2004136//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, In unordered pieces //8.2E-202//926bp//100%//AL096820
 40 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR //9.3E-15//126aa//39%//P38120
 C-NT2RP2004392//MNN4 PROTEIN //1.4E-11//143aa//27%//P36044
 C-NT2RP2004463
 45 C-NT2RP2004602
 C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds./0//2040bp//99%//AB023139
 C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein //8.5E-233//1061bp//99%//AJ006291
 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1 //5.6E-64//616aa//33%//Q92355
 50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS) //9.5E-73//153aa//59%//Q10490
 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) //3.7E-135//414aa//62%//P53588
 C-NT2RP2004802
 55 C-NT2RP2004841
 C-NT2RP2004936
 C-NT2RP2004959//P54 PROTEIN PRECURSOR //0.00000095//297aa//20%//P13692
 C-NT2RP2004999

C-NT2RP2005000
C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds./0//1694bp//99%//AB014515
C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein./0//1693bp//99%//AJ011779
C-NT2RP2005037//ANTI-SILENCING PROTEIN 1//3.3E-47//155aa//59%//P32447
5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//
X9B743
C-NT2RP2005140
C-NT2RP2005147
C-NT2RP2005159
10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds./0//2087bp//99%//AF097025
C-NT2RP2005270
C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds./0//2122bp//99%//D89053
C-NT2RP2005293
C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds./0//1515bp//99%//AB014576
15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds./0//2199bp//99%//AF072247
C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823
C-NT2RP2005436//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPlicing FACTOR SRP75).//1.2E-13//185aa//38%//Q08170
20 C-NT2RP2005441
C-NT2RP2005453
C-NT2RP2005464
C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127
C-NT2RP2005472
25 C-NT2RP2005495
C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//86%//P36876
C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds./0//1825bp//99%//AF151803
C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds./0//
30 3994bp//99%//AF092563
C-NT2RP2005525//Mus musculus kanadapin mRNA, complete cds./2.4E-304//1687bp//85%//AF035526
C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds./0//2856bp//99%//AB007963
C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGlyOXALASE) (AL-DOKEATOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE
35 METHYLGlyOXAL LYASE).//2E-20//181aa//36%//Q39366
C-NT2RP2005555
C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds./1E-46//576bp//70%//AF062529
C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds./8.9e-313//1455bp//98%//AF062085
40 C-NT2RP2005622
C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(*) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//
P47623
C-NT2RP2005637
C-NT2RP2005640
45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56101
C-NT2RP2005669//Homo sapiens mRNA for DEDD protein./3.9E-209//957bp//99%//AJ010973
C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds./4.4E-200//908bp//
99%//AF089814
C-NT2RP2005683
50 C-NT2RP2005690
C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds./0//1684bp//99%//AB018342
C-NT2RP2005723//HNRNP ARGinine N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//
0.00000003//169aa//28%//P38074
C-NT2RP2005748
55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds./0//1968bp//99%//
AF068868
C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds./0//1966bp//99%//
AF082516

- C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943
 C-NT2RP2005767//G. gallus PB1 gene.//5E-163//1158bp//81%//X90849
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//
 2.7E-180//656bp//99%//AF151351
 5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-
 CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-
 BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038
 C-NT2RP2005781
 C-NT2RP2005804
 10 C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223
 C-NT2RP2005853
 C-NT2RP2005868
 C-NT2RP2005886
 C-NT2RP2005890
 15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837
 C-NT2RP2006038
 C-NT2RP2006043//SPLICING FACTOR, ARGinine/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR
 SRP75).//1.5E-13//185aa//38%//Q08170
 20 C-NT2RP2006052
 C-NT2RP2006069
 C-NT2RP2006071
 C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//
 99%//AL049970
 25 C-NT2RP2006106
 C-NT2RP2006141
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%//AB014554
 C-NT2RP2006196
 C-NT2RP2006200
 30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484
 C-NT2RP2006237
 C-NT2RP2006238
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//
 388aa//32%//P46821
 35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262
 C-NT2RP2006333
 C-NT2RP2006365
 C-NT2RP2006393
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//
 40 0.00000034//50aa//50%//Q61658
 C-NT2RP2006456
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
 C-NT2RP2006467
 C-NT2RP2006472
 45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1)(CYP11G1)(P450-NMB)(OLFACTIVE).//4.2E-134//
 486aa//50%//P24461
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//
 169aa//25%//P09543
 50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708
 C-NT2RP3000072
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164
 C-NT2RP3000220
 C-NT2RP3000251
 55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
 C-NT2RP3000312
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor
 Sp1.//0//1544bp//100%//AJ242978

C-NT2RP3000333
 C-NT2RP3000348
 C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN
 HP0303./.0.00000028//185aa/31%//I025074
 5 C-NT2RP3000359//GTP-AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//
 226aa/92%//P08760
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1
 and Prp6./.0//2072bp/98%//A019219
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18//2.1E-107//206aa/99%//P35293
 10 C-NT2RP3000397//PUTATIVE PRE-MRNA SPlicing FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//
 1.7E-139/679aa/41%//O43143
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds./.0//2364bp//99%//AF071185
 C-NT2RP3000484
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa/27%//P28160
 15 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa/30%//
 P15151
 C-NT2RP3000596//TRICHOHYALIN//2.5E-17//304aa/28%//Q07283
 C-NT2RP3000599
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa/46%//P51523
 20 C-NT2RP3000644
 C-NT2RP3000661
 C-NT2RP3000665
 C-NT2RP3000690
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR./.7E-28//176aa/34%//Q94650
 25 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN./.2.5E-36//417aa/31%//Q61982
 C-NT2RP3000836
 C-NT2RP3000841
 C-NT2RP3000850
 C-NT2RP3000852
 30 C-NT2RP3000859
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds./.6.9E-69/1611bp/61%//U53445
 C-NT2RP3000869
 C-NT2RP3000901
 35 C-NT2RP3000917//Homo sapiens Dhm1-like protein mRNA, complete cds./.0//3199bp//99%//AF064257
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds./.0//
 2.7E-185//585bp//88%//AF015264
 C-NT2RP3000980
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN
 40 STAUFEN./.0.00000006//78aa/48%//P25159
 C-NT2RP3001004
 C-NT2RP3001081
 C-NT2RP3001084
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds./.1.7E-94//787bp//66%//AF087433
 45 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa/40%//P55201
 C-NT2RP3001109
 C-NT2RP3001116
 C-NT2RP3001119
 C-NT2RP3001133
 50 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds./.0//2802bp//99%//AB018305
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein./.0//2732bp//99%//AJ006266
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION./.1.7E-10//
 196aa/27%//P53154
 C-NT2RP3001214
 55 C-NT2RP3001216//CYCLIC I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa/33%//
 P35663
 C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-
 BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa/30%//P80193

C-NT2RP3001236
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1]//1.2E-166//395aa/51%//P14873
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0/2497bp//99%//AB020718
 5 C-NT2RP3001307
 C-NT2RP3001325
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0/1213bp//99%//AB025905
 C-NT2RP3001392
 10 C-NT2RP3001396
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF//1.3E-61//374aa/36%//P49711
 C-NT2RP3001407//SCY1 PROTEIN//0.00000033/143aa/25%//P53009
 C-NT2RP3001420
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT)//1E-16//77aa/46%//O33529
 15 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG//2.7E-10//159aa/33%//O09053
 C-NT2RP3001457
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A//9.1E-13//87aa/43%//P11632
 C-NT2RP3001495//Human oxidoreductase (HHCM56) mRNA, complete cds.//0/1475bp//99%//U13395
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//
 20 0/2295bp//99%//AF064801
 C-NT2RP3001529//SPOOB-ASSOCIATED GTP-BINDING PROTEIN//1E-61//345aa/42%//P20964
 C-NT2RP3001621
 C-NT2RP3001629
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210//6.8E-18//91aa/38%//Q92609
 25 C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12//8.8E-09//132aa/31%//O22468
 C-NT2RP3001676
 C-NT2RP3001679
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE//1.6E-11//348aa/27%//P24733
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN)//7.4E-18//249aa/30%//Q04652
 30 C-NT2RP3001896
 C-NT2RP3001915
 C-NT2RP3001929
 C-NT2RP3003193//ZINC FINGER PROTEIN 135//7.3E-98//269aa/62%//P52742
 C-NT2RP3004466
 35 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//3.3E-113//466aa/42%//
 P34110
 C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0/1520bp//99%//AB014532
 C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0/974bp//95%//AB011126
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0.000000038//
 40 150aa/28%//Q01484
 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0/1770bp//99%//
 AF026445
 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0/1639bp//99%//AB007946
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0/1807bp//99%//JN006266
 45 C-NT2RP3004617//ZINC-BINDING PROTEIN A33//7.2E-75//464aa/35%//Q02084
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0/3972bp//98%//
 AF093097
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)//1.7E-72//254aa/
 45%//P54352
 50 C-NT2RP400008//CHLORINE CHANNEL PROTEIN P64//2.6E-98//239aa/64%//P35526
 C-NT2RP4000051//SYNAPTOMEMAL COMPLEX-PROTEIN SC65//4.9E-51//335aa/37%//Q64375
 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0/3013bp//99%//AB020657
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0/2161bp//99%//AB011538
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100
 55 KD SUBUNIT) //0/728aa//99%//Q10568
 C-NT2RP4000129
 C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, com-
 plete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150
 C-NT2RP4000151
 C-NT2RP4000159
 C-NT2RP4000185
 5 C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds./0//4149bp//99%//AB014600
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//
 P15287
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173
 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//
 55%//P87115
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1)(ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631
 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//
 32%//P26372
 C-NT2RP4000355
 C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds./0//4074bp//99%//AB018281
 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds./0//
 20 4782bp//99%//AF044195
 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-
 77//262aa//54%//O75570
 C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243
 C-NT2RP4000381
 25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738
 C-NT2RP4000415
 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSEIDASE (EC 3.2.1.113)(MAN(9)-AL-
 PHA-MANNOSEIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701
 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//
 30 99%//AL050078
 C-NT2RP4000449
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//
 35 2.5E-37//291aa//38%//P50101
 C-NT2RP4000480
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (mRNA TRANSPORT REGULATOR MTR4).//
 1.9E-67//721aa//29%//Q09475
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484
 40 C-NT2RP4000500
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818
 C-NT2RP4000524
 C-NT2RP4000541
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319
 45 C-NT2RP4000560
 C-NT2RP4000588
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds./2.9E-188//863bp//
 99%//AF067730
 C-NT2RP4000638
 50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//
 30%//P39625
 C-NT2RP4000704
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//
 55 Q11073
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267
 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds./0//3392bp//95%//AB023148
 C-NT2RP4000737

C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds./0/3574bp/99%//AB023229
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION./
 0.00000032//67aa//31%//P53915
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds./0/1927bp/99%//AB007939
 5 C-NT2RP4000833
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1./4.3E-94//810bp//65%//Y18265
 C-NT2RP4000839//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1./8.5E-21//271 aa/28%//Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-
 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa/48%//O09175
 10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa/55%//P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN./6.2E-91//173aa/87%//Q35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1SS PROTEIN).//9.6E-96//513aa/42%//P22314
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26/
 227aa//36%//Q06828
 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-
 ZYME 1).//1.5E-76//346aa/43%//Q61068
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein./0//2487bp/99%//Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505./0.00000014//185aa/25%//Q58900
 20 C-NT2RP4000955
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//
 90aa/42%//P38660
 C-NT2RP4000975
 C-NT2RP4000979
 25 C-NT2RP4000984
 C-NT2RP4000989//UNC-47 PROTEIN./0.0000082//173aa//25%//P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
 POLYMERASE I SUBUNIT 2) (RPA135).//0.838aa/87%//P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8./3.7E-16//401aa/26%//P39968
 30 C-NT2RP4001006
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds./0//2482bp/99%//AB023181
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE).//1.5E-
 92//143aa/44%//Q09996
 C-NT2RP4001057
 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65./6.7E-51//335aa/37%//Q64375
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA²⁺-ATPASE).//1.3E-123//
 563aa//46%//P13586
 C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds./0//1439bp/99%//AB023967
 C-NT2RP4001086
 40 C-NT2RP4001095//DOUBLE-STANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-) (DSRNA ADENOSINE DEAM-
 INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa/36%//P51400
 C-NT2RP4001100
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT./1.9E-115//224aa//100%//
 P38378
 45 C-NT2RP4001122//TIPD PROTEIN./1.4E-65//253aa/41%//O15736
 C-NT2RP4001126//TRICHOHYALIN./2.9E-18//380aa//26%//Q07283
 C-NT2RP4001138
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//0.00000021//
 93aa//33%//P44514
 50 C-NT2RP4001148//SOF1 PROTEIN./1.3E-104//236aa/52%//P33750
 C-NT2RP4001149
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//
 3.4E-29//385aa/29%//P35331
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTP).//
 55 4.7E-29//227aa/35%//P52178
 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds./4.4E-104//1460bp//
 65 %//U95760
 C-NT2RP4001207

C-NT2RP4001210
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//
 90aa//42%/P38660
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%//Q04652
 5 C-NT2RP4001235
 C-NT2RP4001256
 C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%//AB020682
 C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%//U49082
 C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%//Q07283
 10 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%//P24391
 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5//8.5E-213//1129bp//92%//
 AJ001119
 C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp//99%//AJ007014
 15 C-NT2RP4001343
 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310//
 1400bp//100%//AB017494
 C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds.//1.4E-58//2425bp//59%//U53445
 20 C-NT2RP4001353
 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-
 19//223aa//30%//Q008180
 C-NT2RP4001373
 C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PRO-
 25 TEIN KINASE 1).//9.2E-17//146aa//35%//P18160
 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2E-53//436aa//30%//
 Q10085
 C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%//AB023140
 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q14141
 30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%//Q999676
 C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%//
 AF129131
 C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-
 PHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
 35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%//P39010
 C-NT2RP4001502
 C-NT2RP4001507
 C-NT2RP4001524
 C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-
 40 54//242aa//3 8%//P25656
 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mR-
 NA, complete cds.//0//3202bp//99%//AF152961
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%//P96902
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26%//Q02453
 45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197
 C-NT2RP4001571
 C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%//AF100756
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//
 50 1.7E-14//373aa//47%//P73505
 C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%//AB020676
 C-NT2RP4001614
 C-NT2RP4001634
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%//P40469
 55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%//P25323
 C-NT2RP4001677
 C-NT2RP4001679
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

100 KD SUBUNIT).//4E-10//243aa//25%//Q10588
C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%//
Q10282
C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)
(DUGT).//6.4E-170//1168aa//33%//Q09332
C-NT2RP4001739
C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%//
P51523
C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
10 CIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174
C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232
C-NT2RP4001803
C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-
15 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//O35566
C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083
C-NT2RP4001828
C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555.bp//73%//
AF155595
C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709
20 C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%//
AL050390
C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000014//345aa//25%//Q00808
C-NT2RP4001901
C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YT1M.//1.3E-38//258aa//32%//Q12024
25 C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711
C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-
ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-
ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816
30 C-NT2RP4001953
C-NT2RP4001966
C-NT2RP4001975
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652
C-NT2RP4002052
35 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//1E-
13//679aa//40%//O43143
C-NT2RP4002071
C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//
39%//Q05481
40 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19
SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%//P52655
C-NT2RP4002298
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938
C-NT2RP4002791
45 C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F172 (from clone DKFZp434F172).//0//2557bp//99%//
AL080202
C-NT2RP4002905
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552
C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808
50 C-NT2RP5003492
C-NT2RP5003500
C-NT2RP5003506
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//
P37116
55 C-NT2RP5003524
C-NT2RP5003534
C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%//

O14727
 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds //2.6E-295//1393bp//97%//AF058922
 C-OVARC1000035
 C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//
 5 0.00000032//60aa//45 %//P80022
 C-OVARC1000087//HISTONE MACRO-H2A.1//1.6E-12//174aa//26%//Q02874
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//
 8.4E-14//259aa//30%//P51610
 C-OVARC1000113
 10 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds //0//1562bp//99%//AF132955
 C-OVARC1000148
 C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//
 2.5E-95//461bp//98%//AJ242975
 C-OVARC1000168
 15 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds //1.8E-32//511bp//65%//
 AF068332
 C-OVARC1000212
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)
 (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665
 20 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-
 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa//
 30%//P14904
 C-OVARC1000304//PROTEIN MOV-10//1.1E-249//519aa//87%//P23249
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363
 25 C-OVARC1000321
 C-OVARC1000326
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//
 200aa//27%//P40004
 C-OVARC1000347
 30 C-OVARC1000384
 C-OVARC1000411
 C-OVARC1000420
 C-OVARC1000437//TENSIN //7.9E-181//340aa//84%//Q04205
 C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp//
 35 99%//AL080126
 C-OVARC1000461
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7 //1.2E-25//227aa//25%//P11075
 C-OVARC1000466
 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
 40 CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452
 C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds //0//1919bp//99%//AB020636
 C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds //2.2E-157//892bp//91 %//AF051850
 C-OVARC1000564
 C-OVARC1000576
 45 C-OVARC1000588
 C-OVARC1000605
 C-OVARC1000640
 C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, com-
 plete cds //0//1812bp//98%//D43772
 50 C-OVARC1000661
 C-OVARC100071//RAS-RELATED PROTEIN RAB-2 //1.1E-46//121aa//79%//P08886
 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933 //1.2E-17//127aa//33%//Q58343
 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds //1.5E-178//1113bp//86%//AF001533
 C-OVARC1001038//Homo sapiens mRNA for Arriadne-2 protein //0//1172bp//97%//AL130978
 55 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds //1E-215//1027bp//98%//AF132946
 C-OVARC1001162
 C-OVARC1001243
 C-OVARC1001296